(54) Title: TNF-α BINDING MOLECULES

(57) Abstract: The present invention relates to TNF-α binding molecules and nucleic acid sequences encoding TNF-α binding molecules. In particular, the present invention relates to TNF-α binding molecules with a high binding affinity, a high association rate, a low dissociation rate with regard to human TNF-α and that are capable of neutralizing TNF-α at low concentrations. Preferably, the TNF-α binding molecules of the present invention comprise light and/or heavy chain variable regions with fully human frameworks (e.g. human germline frameworks).

TNF-α BINDING MOLECULES

The present application claims priority to both U.S. Application Serial Number 10/338,552, filed January 8, 2003, and U.S. Application Serial Number 10/338,627, filed
5   January 8, 2003.

FIELD OF THE INVENTION

The present invention relates to TNF-α binding molecules and nucleic acid sequences encoding TNF-α binding molecules. In particular, the present invention relates to
10 TNF-α binding molecules with a high binding affinity, a high association rate, a low dissociation rate with regard to human TNF-α, and that are capable of preventing TNF-α mediated cytotoxicity at low concentrations. Preferably, the TNF-α binding molecules of the present invention comprise light and/or heavy chain variable regions with fully human frameworks (e.g. human germline frameworks).

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BACKGROUND OF THE INVENTION

Tumor necrosis factor alpha (TNF-α) is a cytokine produced by numerous cell types, including monocytes and macrophages, that was originally identified based on its ability to induce the necrosis of certain mouse tumors. Subsequently, a factor termed cachectin,
20 associated with cachexia, was shown to be identical to TNF-α. TNF-α has been implicated in the pathophysiology of a variety of other human diseases and disorders, including shock, sepsis, infections, autoimmune diseases, transplant rejection and graft-versus-host disease.

Because of the harmful role of human TNF-α (hTNF-α) in a variety of human disorders, therapeutic strategies have been designed to inhibit or counteract hTNF-α
25 activity. In particular, antibodies that bind to, and neutralize, hTNF-α have been sought as a means to inhibit hTNF-α activity. Some of the earliest of such antibodies were mouse monoclonal antibodies (mAbs), secreted by hybridomas prepared from lymphocytes of mice immunized with hTNF-α (see e.g., U.S. Pat. No. 5,231,024 to Moeller et al.). While these mouse anti-hTNF-α antibodies often displayed high affinity for hTNF-α and were able to
30 neutralize hTNF-α activity, their use in vivo has been limited by problems associated with the administration of mouse antibodies to humans, such as a short serum half-life, an inability to trigger certain human effector functions, and elicitation of an unwanted immune response against the mouse antibody in a human (the "human anti-mouse antibody" (HAMA) reaction).

In an attempt to overcome the problems associated with the use of fully murine antibodies in humans, murine anti-hTNF-α antibodies have been genetically engineered to be more "human-like." For example, chimeric antibodies, in which the variable regions of the antibody chains are murine-derived and the constant regions of the antibody chains are

5   human-derived, have been prepared (e.g., U.S. Pat. 5,698,195, herein incorporated by reference). Additionally, humanized antibodies, in which the hypervariable domains and a number of the framework residues of the antibody variable regions are murine-derived but the remainder of the variable regions and the antibody constant regions are human-derived, have also been prepared (e.g. U.S. Pat. 5,994,510 to Adair et al., herein incorporated by

10   reference). However, because these antibodies still retain a substantial number of murine residues, they still may elicit an unwanted immune reaction, the human anti-chimeric antibody (HACA) reaction, especially when administered for prolonged periods (see e.g., Elliott, et al., (1994) Lancet 344:1125-1127; and Elliot, et al., (1994) Lancet 344:1105-1110).

15   Attempts have been made to further limit or eliminate the presence of murine sequences in anti-TNF-α antibodies. For example, human monoclonal autoantibodies against hTNF-α have been prepared using human hybridoma techniques (e.g., U.S. Pat. 5,654,407 to Boyle, herein incorporated by reference). However, these hybridoma-derived monoclonal autoantibodies were reported to have an affinity for hTNF-α that was too low to

20   measure by conventional methods, were unable to bind soluble hTNF-α and were unable to neutralize hTNF-α-induced cytotoxicity (see Boyle, et al., (1993) Cell. Immunol. 152:556-581). Moreover, the success of the human hybridoma technique generally depends upon the natural presence in human peripheral blood of lymphocytes producing autoantibodies specific for hTNF-α.

25   An alternative to naturally-occurring human anti-hTNF-α antibodies would be a recombinant hTNF-α antibody. Recombinant human antibodies that bind hTNF-α with relatively low affinity (i.e., K_d of about 10^{-7} M) and a relatively fast dissociation rate (i.e., k_{off} of about 10^{-2} s^{-1}) have been described (Griffiths, A. D., et al. (1993) EMBO J. 12:725-734). However, because of their relatively fast dissociation kinetics, and relatively low

30   affinity, these antibodies may not be suitable for therapeutic use. Additionally, recombinant human anti-hTNF-α antibodies with moderate binding affinities (K_d of about 6×10^{-10} M), dissociation rates (k_{off} of about 8.8×10^{-5} s^{-1}), association rates (k_{on} of about 1.9×10^5 $M^{-1} s^{-1}$), and neutralization potential (IC_{50} of about 1.25×10^{-10}) have been described (See, D2E7 antibody in U.S. Pat. 6,258,562, herein incorporated by reference).

Accordingly, what is needed, are TNF-α binding molecules with a high binding affinity, a high association rate, a low dissociation rate and improved neutralization properties with regard to human TNF-α, as well as TNF-α binding molecules with significantly reduced immunogenicity in humans.

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SUMMARY OF THE INVENTION

The present invention provides TNF-α binding molecules and nucleic acid sequences encoding TNF-α binding molecules. In particular, the present invention provides TNF-α binding molecules with a high binding affinity, a high association rate, a low

10   dissociation rate with regard to human TNF-α, and enhanced neutralization properties in vitro and in vivo. Preferably, the TNF-α binding molecules of the present invention comprise light and/or heavy chain variable regions with fully human frameworks. In particularly preferred embodiments, the TNF-α binding molecules of the present invention comprise light and/or heavy chain variable regions with germline frameworks (e.g. human

15   germline frameworks).

In some embodiments, the present invention provides compositions comprising a peptide, or a nucleic acid sequence encoding a peptide, wherein the peptide comprises an amino acid sequence selected from SEQ ID NOs: 11, 13, and 15. In other embodiments, the peptide further comprises one or more amino acid sequences selected from SEQ ID NOs:

20   19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, and 55.

In certain embodiments, the present invention provides compositions comprising a peptide, or a nucleic acid sequence encoding a peptide, wherein the peptide comprises an amino acid sequence selected from SEQ ID NOs: 21, 25, and 27. In other embodiments, the peptide further comprises one or more amino acid sequences selected from SEQ ID NOs: 9,

25   11, 13, 15, 17, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53 and 55.

In additional embodiments, the present invention provides compositions comprising a peptide, or a nucleic acid sequence encoding a peptide, wherein the peptide comprises an amino acid sequence shown in SEQ ID NO: 33. In certain embodiments, the peptide further comprises one or more amino acid sequences selected from SEQ ID NOs: 9, 11, 13, 15, 17,

30   19, 21, 23, 25, 27, 29, 31, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, and 55.

In some embodiments, the present invention provides compositions comprising a peptide, or a nucleic acid sequence encoding a peptide, wherein the peptide comprises an amino acid sequence selected from SEQ ID NOs: 35, 37, and 39. In other embodiments, the

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peptide further comprises one or more amino acid sequences selected from SEQ ID NOs: 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 43, 45, 47, 49, 51, 53, and 55.

In particular embodiments, the present invention provides compositions comprising a peptide, or a nucleic acid sequence encoding a peptide, wherein the peptide comprises an

5   amino acid sequence selected from SEQ ID NOs: 45 and 49. In other embodiments, the peptide further comprises one or more amino acid sequences selected from SEQ ID NOs: 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, and 53.

In certain embodiments, the present invention provides compositions comprising a peptide, or a nucleic acid sequence encoding a peptide, wherein the peptide comprises an

10 amino acid shown in SEQ ID NO: 53. In additional embodiments, the peptide further comprises one or more amino acid sequences selected from SEQ ID NOs: 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, and 55.

In particular embodiments, the present invention provides compositions comprising a peptide, or a nucleic acid sequence encoding a peptide, wherein the peptide comprises an

15 amino acid sequences selected from SEQ ID NOs:87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107 and 109.

In some embodiments, the TNF-α binding molecule is a TNF-α binding peptide or polypeptide. In certain embodiments, the TNF-α binding peptide comprises an anti-TNF-α antibody or anti-TNF-α antibody fragment (e.g., Fab, F(ab')$_2$, etc). In other embodiments,

20 the peptide comprises a light and/or heavy chain variable region. In particular embodiments, the light chain variable region and/or heavy chain variable region comprises a framework region. In certain embodiments, at least FRL1, FRL2, FRL3, or FRL4 is fully human. In other embodiments, at least FRH1, FRH2, FRH3, or FRH4 is fully human. In some embodiments, at least FRL1, FRL2, FRL3, or FRL4 is a germline sequence (e.g.

25 human germline). In other embodiments, at least FRH1, FRH2, FRH3, or FRH4 is a germline sequence (e.g. human germline). In preferred embodiments, the framework region is a fully human framework region (e.g. the human framework regions shown in Figures 5 and 6). In some embodiments, the framework region comprises SEQ ID NO: 57, 58, 59, 60 or combinations thereof. In other embodiments, the framework region comprises SEQ ID

30 NO: 65, 66, 67, 68, or combinations thereof.

In some embodiments, the present invention provides compositions comprising an oligonucleotide, wherein the oligonucleotide comprises a nucleic acid sequence selected from SEQ ID NO: 12, 14, or 16. In other embodiments, the oligonucleotide further

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comprises one or more nucleic acid sequences selected from SEQ ID NOs: 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, and 56.

In certain embodiments, the present invention provides compositions comprising an oligonucleotide, wherein the oligonucleotide comprises a nucleic acid sequence selected from SEQ ID NOs: 22, 26, and 28. In further embodiments, the oligonucleotide further comprises one or more nucleic acid sequences selected from SEQ ID NOs: 10, 12, 14, 16, 18, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, and 54.

In other embodiments, the present invention provides compositions comprising an oligonucleotide, wherein the oligonucleotide comprises a nucleic acid sequence shown in SEQ ID NO:34. In certain embodiments, the oligonucleotide further comprises one or more nucleic acid sequences selected from SEQ ID NOs: 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 36, 38, 40, 42, 44, 46, 48, 50, 52 and 54.

In particular embodiments, the present invention provides compositions comprising an oligonucleotide, wherein the oligonucleotide comprises a nucleic acid sequence selected from SEQ ID NOs: 36, 38, and 40. In additional embodiments, the oligonucleotide further comprises one or more nucleic acid sequences selected from SEQ ID NOs: 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 44, 46, 48, 50, 52, and 54.

In other embodiments, the present invention provides compositions comprising an oligonucleotide, wherein the oligonucleotide comprises a nucleic acid sequence selected from SEQ ID NOs: 46 and 50. In some embodiments, the oligonucleotide further comprises one or more nucleic acid sequences selected from SEQ ID NOs: 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, and 54.

In additional embodiments, the present invention provides compositions comprising an oligonucleotide, wherein the oligonucleotide comprises a nucleic acid sequence shown in SEQ ID NO:54. In certain embodiments, the oligonucleotide further comprises one or more nucleic acid sequences selected from SEQ ID NOs: 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, and 52.

In some embodiments, the oligonucleotide further comprises a vector sequence. In other embodiments, the oligonucleotide further comprises a nucleic acid sequence encoding an antibody variable region framework. In preferred embodiments, the framework is fully human. In additional embodiments, the oligonucleotide further comprises a nucleic acid sequence encoding an antibody constant region. In some embodiments, the oligonucleotide comprises a framework region selected from SEQ ID NO: 61, 62, 63, 64, 69, 70, 71, 72, or combinations thereof. In certain embodiments, the human germline light and/or heavy

chain frameworks shown in Figure 15 are employed (i.e. IGKV1-39 for the light chain, and IGVH3-72 for the heavy chain).

In some embodiments, the present invention provides compositions comprising a TNF-α binding molecule, or an oligonucleotide encoding a TNF-α binding molecule,
5   wherein the TNF-α binding molecule comprises: i) a CDRL3 sequence comprising SEQ ID NO: 33, and ii) a CDRH3 comprising SEQ ID NO: 53. In particular embodiments, the TNF-α molecule comprises the hu1 Fab (e.g., an IgG with the variable regions present in the hu1 Fab fragment).

In certain embodiments, the TNF-α binding molecule further comprises iii) a
10 CDRL1 sequence comprising SEQ ID NO: 11, and iv) a CDRL2 sequence comprising SEQ ID NO:21. In other embodiments, the TNF-α binding molecule further comprises: v) a CDRH1 sequence comprising SEQ ID NO: 37, and vi) a CDRH2 sequence comprising SEQ ID NO: 49. In some embodiments, the TNF-α binding molecule comprises the 2C6K Fab (e.g., an IgG with the variable regions present in the 2C6K Fab fragment). In additional
15 embodiments, the TNF-α binding molecule further comprises: v) a CDRH1 sequence comprising SEQ ID NO: 39, and vi) a CDRH2 sequence comprising SEQ ID NO: 49. In particular embodiments, the TNF-α binding molecule comprises the 2C6P Fab (e.g., an IgG with the variable regions present in the 2C6P Fab fragment).

In some embodiments, the TNF-α binding molecule further comprises: iii) a CDRL1
20 sequence comprising SEQ ID NO: 11, and iv) a CDRL2 sequence comprising SEQ ID NO: 25. In other embodiments, the TNF-α binding molecule further comprises: v) a CDRH1 sequence comprising SEQ ID NO: 37, and vi) a CDRH2 sequence comprising SEQ ID NO: 55. In particular embodiments, the TNF-α binding molecule comprises the 2E7K Fab (e.g., an IgG with the variable regions present in the 2E7K Fab fragment). In other embodiments,
25 the TNF-α binding molecule further comprises: v) a CDRH1 sequence comprising SEQ ID NO: 39, and vi) a CDRH2 sequence comprising SEQ ID NO: 55. In particular embodiments, the TNF-α binding molecule comprises the 2E7P Fab (e.g., an IgG with the variable regions present in the 2E7P Fab fragment).

In additional embodiments, the TNF-α binding molecule further comprises: iii) a
30 CDRL1 sequence comprising SEQ ID NO: 13, and iv) a CDRL2 sequence comprising SEQ ID NO: 27. In some embodiments, the TNF-α binding molecule further comprises: v) a CDRH1 sequence comprising SEQ ID NO: 37, and vi) a CDRH2 sequence comprising SEQ ID NO: 55. In particular embodiments, the TNF-α binding molecule comprises the A9K Fab (e.g., an IgG with the variable regions present in the A9K Fab fragment). In certain

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embodiments, the TNF-α binding molecule further comprises: v) a CDRH1 sequence comprising SEQ ID NO: 39, and vi) a CDRH2 sequence comprising SEQ ID NO: 55. In particular embodiments, the TNF-α binding molecule comprises the A9P Fab (e.g., an IgG with the variable regions present in the A9P Fab fragment).

5   In some embodiments, the TNF-α binding molecule further comprises: iii) a CDRL1 sequence comprising SEQ ID NO: 15, and iv) a CDRL2 sequence comprising SEQ ID NO: 25. In other embodiments, the TNF-α binding molecule further comprises: v) a CDRH1 sequence comprising SEQ ID NO: 37, and vi) a CDRH2 sequence comprising SEQ ID NO: 45. In particular embodiments, the TNF-α binding molecule comprises the A10K Fab (e.g.,

10   an IgG with the variable regions present in the A10K Fab fragment). In other embodiments, the TNF-α binding molecule further comprises: v) a CDRH1 sequence comprising SEQ ID NO: 39, and vi) a CDRH2 sequence comprising SEQ ID NO: 45. In particular embodiments, the TNF-α binding molecule comprises the A10P Fab (e.g., an IgG with the variable regions present in the A10P Fab fragment).

15   In some embodiments, the TNF-α binding molecule further comprises: iii) a CDRL1 sequence comprising SEQ ID NO: 9, and iv) a CDRL2 sequence comprising SEQ ID NO: 19. In other embodiments, the TNF-α binding molecule further comprises: v) a CDRH1 sequence comprising SEQ ID NO: 35, and vi) a CDRH2 sequence comprising SEQ ID NO:43.

20   In certain embodiments, the TNF-α binding molecule further comprises a light chain variable region, wherein the light chain variable region comprises a framework region. In some embodiments, the light chain variable region comprises light chain framework regions selected from SEQ ID NOs: 57, 58, 59, 60, and combinations thereof. In preferred embodiments, the framework region is a fully human framework. In particularly preferred

25   embodiments, the framework region is a germline framework (e.g. human or other animal germline framework).

In some embodiments, the TNF-α binding molecule further comprises a heavy chain variable region, wherein the heavy chain variable region comprises a framework region. In certain embodiments, the heavy chain variable region comprises a heavy chain framework

30   regions selected from SEQ ID NOs: 65, 66, 67, 68, and combinations thereof. In preferred embodiments, the framework is a fully human framework. In particularly preferred embodiments, the framework region is a germline framework (e.g. human or other animal germline framework).

In certain embodiments, the present invention provides compositions comprising a light chain variable region, or a nucleic acid sequence encoding a light chain variable region, wherein the light chain variable region comprises an amino acid sequence selected from SEQ ID NOs:1 and 5. In other embodiments, the present invention provides compositions comprising an oligonucleotide encoding a light chain variable region, wherein the oligonucleotide comprises SEQ ID NO: 2 or SEQ ID NO: 6.

In some embodiments, the present invention provides compositions comprising a heavy chain variable region, or a nucleic acid sequence encoding a heavy chain variable region, wherein the heavy chain variable region comprises an amino acid sequence selected from SEQ ID NOs: 3 and 7. In particular embodiments, the present invention provides compositions comprising an oligonucleotide encoding a heavy chain variable region, wherein the oligonucleotide comprises SEQ ID NO: 4 or SEQ ID NO: 8.

In some embodiments, the present invention provides a computer readable medium that encodes a representation of a nucleic acid or amino acid sequence selected from SEQ ID NOs: 1-108, or the complement thereof. In certain embodiments, the representation of these sequences, when delivered to a computer processor, may be displayed to a user (e.g., over the internet). In particular embodiments, the present invention provide the complement of the CDR encoding nucleic acid sequences described herein (e.g. SEQ ID NOs:10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 74, 76, 78, 80, 82, 84, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, and 108). In additional embodiments, the present invention provides nucleic acid sequences that will hybridize (under low, medium or high stringency conditions) to the CDR encoding nucleic acid sequences described herein (e.g. SEQ ID NOs:10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 74, 76, 78, 80, 82, 84, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, and 108).

In some embodiments, the present invention provides the complement of the nucleic acid sequences described herein (see e.g. Tables 1-3 and 6). In some embodiments, the present invention provides sequences that hybridize under high, medium or low stringency with the nucleic acid sequences described herein (see e.g. Tables 1-3, and 6).

In certain embodiments, the present invention provides compositions comprising a TNF-α binding molecule that has an association rate constant (k_{on}) for human TNF-α of 3.0 x 10^6 M^{-1} s^{-1} or greater. In other embodiments, the association rate constant is 4.0 x 10^6 M^{-1} s^{-1} or greater (e.g., about 4.1 x 10^6 M^{-1} s^{-1}, about 5.5 x 10^6 M^{-1} s^{-1}, or about 7.0 x 10^6 M^{-1} s^{-1}). In other embodiments, the association rate constant is between about 3.0 x 10^6 M^{-1} s^{-1} and

about $7.5 \times 10^6 \, M^{-1} \, s^{-1}$ (e.g., between about $3.5 \times 10^6 \, M^{-1} \, s^{-1}$ and about $7.0 \times 10^6 \, M^{-1} \, s^{-1}$, or between about $4.0 \times 10^6 \, M^{-1} \, s^{-1}$ and about $6.0 \times 10^6 \, M^{-1} \, s^{-1}$).

In some embodiments, the association rate constant is determined by a kinetic exclusion assay (See, e.g., Chiu et al., (2001) Anal. Chem., 73:5477-5484; Blake, et al., (1996) Journal of Biological Chemistry, 271:27677-27685; Hongo, et al., (2000) Hybridoma, 19:303-315; Khosraviani, et al., (2000) Bioconjugate Chemistry, 11:267-277; and Powers, et al., (2001) Journal of Immunological Methods, 251:123-135, all of which are herein incorporated by reference). In particular embodiments, the kinetic exclusion assay is performed with a KinExA instrument (e.g., KinExA™3000 from Sapidyne Instruments, Boise, Idaho), or similar device.

In further embodiments, the TNF-α binding molecule has a binding affinity (K_d) for human TNF-α of about 7.5×10^{-12} M or less. In other embodiments, the binding affinity is about 5.0×10^{-12} M or less. In certain embodiments, the binding affinity is about 3.0×10^{-12} M or less. In some embodiments, the binding affinity is 2.2×10^{-12} M or less. In yet other embodiments, the binding affinity is between about 7.2×10^{-12} M and about 2.0×10^{-12} M (e.g., between about 6.0×10^{-12} M and about 3.0×10^{-12} M, or between about 5.0×10^{-12} M and about 4.0×10^{-12} M). In particular embodiments, the binding affinity is determined by a kinetic exclusion assay (e.g., with a KinExA instrument).

In certain embodiments, the TNF-α binding molecule has a dissociation rate constant (k_{off}) for human TNF-α of about $1.0 \times 10^{-4} \, s^{-1}$ or less. In some embodiments, the dissociation rate constant is about $1.0 \times 10^{-5} \, s^{-1}$ or less, about $9.0 \times 10^{-6} \, s^{-1}$ or less, or about $7.0 \times 10^{-6} \, s^{-1}$ or less. In other embodiments, the dissociation rate constant is between about $1.0 \times 10^{-4} \, s^{-1}$ and about $8.0 \times 10^{-6} \, s^{-1}$ (e.g., between about $1.0 \times 10^{-5} \, s^{-1}$ and about $6.0 \times 10^{-6} \, s^{-1}$). In certain embodiments, the dissociation rate is determined by a kinetic exclusion assay.

In some embodiments, the present invention provides compositions comprising a TNF-α binding molecule that neutralizes human TNF-α cytotoxicity in an in vitro, cell-based assay (see, e.g., Example 2) with an EC_{50} of 1.0×10^{-10} or less (e.g., 1.0×10^{-10} - 1.0×10^{-11}). In other embodiments, the TNF-α binding molecule neutralizes human TNF-α cytotoxicity in an in vitro, cell-based assay with an EC_{50} of 7.0×10^{-11} or less (e.g., 7.0×10^{-11} - 3.0×10^{-11}). In some embodiments, the TNF-α binding molecule neutralizes human TNF-α cytotoxicity in an in vitro, cell-based assay with an EC_{50} of 2.0×10^{-12} or less (e.g., 1.9×10^{-12} or less, 1.8×10^{-12} or less, 1.7×10^{-12} or less, 1.6×10^{-12} or less, 1.5×10^{-12} or less, 1.4×10^{-12} or less, 1.3×10^{-12} or less, 1.2×10^{-12} or less, 1.1×10^{-12} or less, 1.0×10^{-12}

or less, 0.9×10^{-12} or less, 0.8×10^{-12} or less, etc.). In additional embodiments, the TNF-α

binding molecule neutralizes human TNF-α cytotoxicity in an in vitro, cell-based assay with

an EC_{50} of 3.0×10^{-12} or less (e.g., 3.0×10^{-12} - 2.0×10^{-12}). In particular embodiments, the

neutralization assay is performed by treating L929 mouse fibroblasts with the molecules of

5   the present invention and subsequently determining an effective concentration capable of

preventing TNF-α mediated cell death.

        In some embodiments, the TNF-α binding molecule comprises a light chain variable

region and a heavy chain variable region. In certain embodiments, the light chain variable

region comprises a fully human framework (see, e.g., Figure 5). In some embodiments, the

10   light chain variable region comprises a germline framework (e.g. human germline

framework). In other embodiments, the heavy chain variable region comprises a fully

human framework (see, e.g., Figure 6). In additional embodiments, the heavy chain

variable region comprises a germline framework (e.g. human germline framework). In

certain embodiments, the human germline light and/or heavy chain frameworks shown in

15   Figure 15 are employed (i.e. IGKV1-39 for the light chain, and IGVH3-72 for the heavy

chain).

        In particular embodiments, the TNF-α binding molecule comprises a Fab or F(ab')₂.

In other embodiments, the TNF-α binding molecule comprises a Fab, and further comprises

one or more constant regions (e.g., CH2 and/or CH3, see Figure 13). In particular

20   embodiments, the TNF-α binding molecule comprises an antibody (e.g., an antibody

comprising a fully human framework with synthetic CDR sequences). In certain

embodiments, the antibody comprises an altered (e.g., mutated) Fc region. For example, in

some embodiments, the Fc region has been altered to reduce or enhance the effector

functions of the antibody. In some embodiments, the Fc region is an isotype selected from

25   IgM, IgA, IgG, IgE, or other isotype.

        In some embodiments, the present invention provides compositions comprising a

TNF-α binding molecule, or a nucleic acid sequence encoding a TNF-α binding molecule,

wherein said TNF-α binding molecule comprises at least one of the following CDR

sequences; i) a CDRL1 sequence comprising SEQ ID NO:93; ii) a CDRL2 sequence

30   comprising SEQ ID NO:95; iii) a CDRL3 sequence comprising SEQ ID NO: 97; iv) a

CDRH1 sequence comprising SEQ ID NO:87; v) a CDRH2 sequence comprising SEQ ID

NO:89, and vi) a CDRH3 sequence comprising SEQ ID NO: 91. In other embodiments, the

TNF-α binding molecule comprises at least two, or at least three, or at least four, or at least

five of the CDR sequences. In some embodiments, the TNF-α binding molecule comprises

all six of the CDR sequences. In certain embodiments, the TNF-α binding molecule comprises a heavy chain sequences as shown in SEQ ID NO:109 (See Figure 15). In other embodiments, the TNF-α binding molecule comprises a light chain sequences as shown in SEQ ID NO:110 (See Figure 15). In preferred embodiments, the TNF-α binding molecule

5   is AME 3-2 and comprises both SEQ ID NO:109 (heavy chain) and SEQ ID NO:110 (light chain).

In some embodiments, amino acid modification(s) are introduced into the CH2 domain of an Fc region of a TNF-α binding molecule. Useful amino acid positions for modification in order to generate a variant IgG Fc region with altered Fc gamma receptor

10   (FcγR) binding affinity or activity include any one or more of the following amino acid positions: 268, 269, 270, 272, 276, 278, 280, 283, 285, 286, 289, 290, 292, 293, 294, 295, 296, 298, 300 301, 303, 305, 307, 309, 331,333, 334, 335, 337, 338, 340, 360, 373, 376, 416, 419, 430, 434, 435, 437, 438 or 439 of the Fc region of a TNF-α binding molecule. In preferred embodiments, the parent Fc region used as the template to generate such variants

15   comprises a human IgG Fc region. In some embodiments, to generate an Fc region variant with reduced binding to the FcγR one may introduce an amino acid modification at any one or more of the following amino acid positions: 252, 254, 265, 268, 269, 270, 272, 278, 289, 292, 293, 294, 295, 296, 298, 300, 301, 303, 322, 324, 327, 329, 333, 335, 338, 340, 373, 376, 382, 388, 389, 414, 416, 419, 434, 435, 437, 438 or 439 of the Fc region of a TNF-α

20   binding molecule. In particular embodiments, Fc region variants with improved binding to one or more FcγRs may also be made. Such Fc region variants may comprise an amino acid modification at any one or more of the following amino acid positions: 280, 283, 285, 286, 290, 294, 295, 298, 300, 301, 305, 307, 309, 312, 315, 331, 333, 334, 337, 340, 360, 378, 398 or 430 of the Fc region of a TNF-α binding molecule.

25   In certain embodiments, the present invention provides TNF-α binding molecules comprising a variant of a parent polypeptide having an Fc region, wherein the variant binds an FcγR with higher affinity than said parent polypeptide, and/or interacts with an FcγR with a higher assay signal, and/or mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the presence of effector cells, and comprises at least one amino acid

30   modification at position 300 in the Fc region. In certain embodiments, the amino acid modification is Y300I. In other embodiments, the amino acid modification is Y300L.

In some embodiments, the present invention provides TNF-α binding molecules comprising a variant of a parent polypeptide having an Fc region, wherein the variant binds an Fc gamma receptor III (FcγRIII) with higher affinity, or the variant interacts with an

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FcγRIII with a higher assay signal, than the parent polypeptide, and/or mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the presence of effector cells, and comprises at least one amino acid modification at position 295 in the Fc region. In certain embodiments, the amino acid modification is Q295K or Q295L.

5   In particular embodiments, the present invention provides TNF-α binding molecules comprising a variant of a parent polypeptide having an Fc region, wherein the variant binds an FcγRIII with higher affinity, or the variant interacts with an FcγRIII with a higher assay signal, than the parent polypeptide, and/or mediates antibody-dependent cell-mediated cytotoxicity (ADCC) in the presence of effector cells, and comprises at least one amino acid

10   modification at position 294 in the Fc region. In certain embodiments, the amino acid modification is E294N.

In other embodiments, the present invention provides TNF-α binding molecules comprising a variant of a parent polypeptide having an Fc region, wherein the variant has a binding affinity, or assay signal, for FcγRII or FcγRIIb that is approximately 0.25 or less as

15   measured in an ELISA FcγR binding assay. In certain embodiments, the variant comprises at least one amino acid modification at position 296 in the Fc region. In particular embodiments, the amino acid modification at position 296 is Y296P. In other embodiments, the variant comprises at least one amino acid modification at position 298 in the Fc region. In some embodiments, the amino acid modification at position 298 is S298P.

20   In particular embodiments, the present invention provides TNF-α binding molecules comprising a variant of a parent polypeptide having an Fc region, wherein the variant binds an FcγRIII with greater affinity, and FcγRIIb with less affinity, than the parent polypeptide and the variant comprises a S298N amino acid modification in the Fc region. In some embodiments, the present invention provides compositions comprising a variant of a parent

25   polypeptide having an Fc region, wherein the variant interacts with an FcγRIII with a higher assay signal, and FcγRIIb with lower assay signal, than the parent polypeptide and the variant comprises a S298N amino acid modification in the Fc region.

In other embodiments, the present invention provides TNF-α binding molecules comprising a variant of a parent polypeptide having an Fc region, wherein the variant binds

30   an FcγRIII with greater affinity, and FcγRIIb with less affinity, than the parent polypeptide and the variant comprises a S298V amino acid modification in the Fc region. In some embodiments, the present invention provides compositions comprising a variant of a parent polypeptide having an Fc region, wherein the variant interacts with an FcγRIII with a higher

assay signal, and FcγRIIb with a lower assay signal, than the parent polypeptide and the variant comprises a S298V amino acid modification in the Fc region.

In some embodiments, the present invention provides TNF-α binding molecules comprising a variant of a parent polypeptide having an Fc region, wherein the variant binds
5   an FcγRIII with greater affinity, and FcγRIIb with less affinity, than the parent polypeptide and the variant comprises a S298D amino acid modification in the Fc region. In other embodiments, the present invention provides compositions comprising a variant of a parent polypeptide having an Fc region, wherein the variant interacts with an FcγRIII with a higher assay signal, and FcγRIIb with a lower assay signal, than the parent polypeptide and the
10   variant comprises a S298D amino acid modification in the Fc region.

In certain embodiments, the present invention provides TNF-α binding molecules comprising a variant of a parent polypeptide having an Fc region, wherein the variant has a binding affinity, or assay signal, for FcγRII or FcγRIIb that is approximately 0.25 or less as measured in an ELISA FcγR binding assay, and wherein the variant comprises at least one
15   amino acid modification at position 298 of the Fc region. In particular embodiments, the amino acid modification at position 298 is S298P.

The polypeptide variants described above may be subjected to further modifications, depending on the desired or intended use of the polypeptide. Such modifications may involve, for example, further alteration of the amino acid sequence (substitution, insertion
20   and/or deletion of amino acid residues), fusion to heterologous polypeptide(s) and/or covalent modifications. Such further modifications may be made prior to, simultaneously with, or following, the amino acid modification(s) disclosed above which result in an alteration of Fc receptor binding and/or ADCC activity.

Alternatively or additionally, it may be useful to combine amino acid modifications
25   with one or more further amino acid modifications that alter C1q binding and/or the complement dependent cytotoxicity function of the Fc region of a TNF-α binding molecule. The starting polypeptide of particular interest may be one that binds to C1q and displays complement dependent cytotoxicity (CDC). Amino acid substitutions described herein may serve to alter the ability of the starting polypeptide to bind to C1q and/or modify its
30   complement dependent cytotoxicity function (e.g., to reduce and preferably abolish these effector functions). However, polypeptides comprising substitutions at one or more of the described positions with improved C1q binding and/or complement dependent cytotoxicity (CDC) function are contemplated herein. For example, the starting polypeptide may be unable to bind C1q and/or mediate CDC and may be modified according to the teachings

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herein such that it acquires these further effector functions. Moreover, polypeptides with pre-existing C1q binding activity, optionally further having the ability to mediate CDC may be modified such that one or both of these activities are enhanced. Amino acid modifications that alter C1q and/or modify its complement dependent cytotoxicity function

5   are described, for example, in WO0042072, which is hereby incorporated by reference.

As disclosed above, one can design an Fc region of a TNF-α binding molecule with altered effector function, e.g., by modifying C1q binding and/or FcγR binding and thereby changing CDC activity and/or ADCC activity. For example, one can generate a variant Fc region of a TNF-α binding molecule with improved C1q binding and improved

10   FcγRIIIbinding (e.g., having both improved ADCC activity and improved CDC activity). Alternatively, where one desires that effector function be reduced or ablated, one may engineer a variant Fc region with reduced CDC activity and/or reduced ADCC activity. In other embodiments, one may increase only one of these activities, and optionally also reduce the other activity (e.g., to generate an Fc region variant with improved ADCC

15   activity, but reduced CDC activity and vice versa).

Fc mutations can also be introduced in the TNF-α binding molecules of the present invention to alter their interaction with the neonatal Fc receptor (FcRn) and improve their pharmacokinetic properties. Several experiments suggest that the interaction between the Fc region of an antibody and the FcRn plays a role in the persistence of immunoglobulins in

20   serum. For instance, an unusually short serum half-life is observed for IgG molecules in mice that lack a functional FcRn. Fc mutations that improve binding to the FcRn appear to prolong serum half-life and, conversely, mutations in the rat FcRn that result in tighter IgG binding also improve serum half-life. A collection of human Fc variants with improved binding to the FcRn has also been described (Shields et al., (2001) High resolution mapping

25   of the binding site on human IgG1 for FcγRI, FcγRII, FcγRIII, and FcRn and design of IgG1 variants with improved binding to the FcγR, J. Biol. Chem. 276:6591-6604). It has been reported that the increased binding affinity of IgG molecules for the FcRn observed at low pH (e.g., during pinocytosis or fluid phase endocytosis of IgG molecules from serum) impacts serum half-life (Ghetie et al., (1997) Increasing the serum persistence of an IgG

30   fragment by random mutagenesis, Nat. Biotechnol. 15:637-640; Medesan et al., (1998) Comparative studies of rat IgG to further delineate the Fc:FcRn interaction site. Eur. J. Immunol. 28:2092-2100; Kim et al., (1999) Mapping the site on human IgG for binding of the MHC class I-related receptor, FcRn, Eur. J. Immunol. 29:2819-2825; Acqua et al., (2002) Increasing the affinity of a human IgG1 for the neonatal Fc receptor: biological

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consequences, J. Immunol. 169:5171-5180). However, mutations that increase binding at high pH appear to adversely affect serum half-life (Acqua et al., (2002) Increasing the affinity of a human IgG1 for the neonatal Fc receptor: biological consequences, J. Immunol. 169:5171-5180). All of the articles above are herein incorporated by reference. Therefore,

5   Fc mutations could be introduced in the TNF-α binding molecules of the present invention in order to increase their affinity for the FcRn at low pH but maintain or decrease their affinity for the FcRn at higher pH.

Another type of amino acid substitution serves to alter the glycosylation pattern of the Fc region of a TNF-α binding molecule. This may be achieved, for example, by

10   deleting one or more glycosylation site(s) found in the polypeptide, and/or adding one or more glycosylation sites that are not present in the polypeptide. Glycosylation of an Fc region is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The peptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline,

15   are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these peptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-aceylgalactosamine, galactose, or xylose to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-

20   hydroxylysine may also be used.

Addition of glycosylation sites to the Fc region of a TNF-α binding molecule is conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tripeptide sequences (for N-linked glycosylation sites). An exemplary glycosylation variant has an amino acid substitution of residue Asn 297 of the

25   heavy chain. The alteration may also be made by the addition of, or substitution by, one or more serine or threonine residues to the sequence of the original polypeptide (for O-linked glycosylation sites).

In some embodiments, the present invention provides methods of treating a TNF-α mediated disease comprising the administration of the TNF-α binding molecules of the

30   present invention to a subject (e.g., a human). In certain embodiments, the administration is under conditions such that the symptoms of the TNF-α mediated disease are reduced or eliminated. In particular embodiments, the TNF-α mediated disease is selected from sepsis, an autoimmune disease, rheumatoid arthritis, allergy, multiple sclerosis, autoimmune uveitis, nephrotic syndrome, an infectious disease, a malignancy, transplant rejection, graft-

versus-host disease, systemic lupus erythematosus, thyroidosis, scleroderma, diabetes mellitus, Graves' disease, a pulmonary disorder, a bone disorder, an intestinal disorder, a cardiac disorder, cachexia, circulatory collapse, shock resulting from acute or chronic bacterial infections, acute and chronic parasitic and/or infectious diseases, chronic

5   inflammatory pathologies, vascular inflammatory pathologies, sarcoidosis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, disseminated intravascular coagulation, atherosclerosis, Kawasaki's pathology, neurodegenerative diseases, demyelinating diseases, multiple sclerosis, acute transverse myelitis, extrapyramidal and cerebellar disorders, lesions of the corticospinal system, disorders of the basal ganglia, hyperkinetic movement

10   disorders, Huntington's chorea, senile chorea, drug-induced movement disorders (e.g., those induced by drugs which block CNS dopamine receptors), hypokinetic movement disorders, Parkinson's disease, progressive supranuclear palsy, spinocerebellar disorders, structural lesions of the cerebellum, spinocerebellar degenerations, spinal ataxia, Friedreich's ataxia, cerebellar cortical degenerations, multiple systems degenerations, Shy-Drager syndrome,

15   Mencel, Dejerine-Sottas, and Machado-Joseph diseases, systemic disorders, Refsum's disease, abetalipoprotemia, ataxia, telangiectasia, mitochondrial multi-system disorder, disorders of the motor unit, neurogenic muscular atrophies, anterior horn cell degeneration, amyotrophic lateral sclerosis, infantile spinal muscular atrophy, juvenile spinal muscular atrophy, Alzheimer's disease, Down's Syndrome, Diffuse Lewy body disease, senile

20   dementia of Lewy body type, Wernicke-Korsakoff syndrome, chronic alcoholism, Creutzfeldt-Jakob disease, subacute sclerosing panencephalitis, Hallerrorden-Spatz disease, dementia pugilistica, malignant pathologies involving TNF-α-secreting tumors or other malignancies involving TNF, such as, leukemias (acute, chronic myelocytic, chronic lymphocytic and/or myelodyspastic syndrome), lymphomas (e.g., Hodgkin's, non-Hodgkin's

25   and Burkitt's lymphomas), mycosis fungoides, alcohol-induced hepatitis, psoriasis, psoriatic arthritis, Wegener's granulomatosis, ankylosing spondylitis, heart failure, reperfusion injury, chronic obstructive pulmonary disease, pulmonary fibrosis, and hepatitis C infection. In preferred embodiments, the TNF-α mediated disease is selected from the group consisting of juvenile and adult rheumatoid arthritis, Crohn's disease, psoriasis, ulcerative

30   colitis, psoriatic arthritis, ankylosing spondylitis, and other spondyloarthropathies, Wegener's granulomatosis, idiopathic pulmonary fibrosis, chronic obstructive pulmonary disease, asthma, oncology, and graft-versus-host disease.

In some embodiments, the TNF-α binding molecule is administered in combination with an immunosuppressant such as methotrexate. In other embodiments, the TNF-α binding molecule is administered intravenously.

In certain embodiments, the present invention provides kits comprising: a) a TNF-α
5   binding molecule of the present invention; and b) instructions for using the TNF-α binding molecule to treat a disease in a subject or instructions for employing the TNF-α binding molecule for scientific research or diagnostic purposes (e.g., for performing ELISA assays, etc.). In some embodiments, the present invention provides cell lines stably or transiently transfected with nucleic acid sequences encoding the TNF-α binding molecules of the
10 present invention.

DESCRIPTION OF THE FIGURES

Figure 1A shows the amino acid sequence of the light chain variable region of hu1 (SEQ ID NO: 1), and Figure 1B shows the nucleic acid sequence of the light chain variable
15 region of hu1 (SEQ ID NO: 2).

Figure 2A shows the amino acid sequence of the heavy chain variable region of hu1 (SEQ ID NO: 3), and Figure 2B shows the nucleic acid sequence of the heavy chain variable region of hu1 (SEQ ID NO: 4).

Figure 3A shows the amino acid sequence of the light chain variable region of A10K
20 (SEQ ID NO: 5), and Figure 3B shows the nucleic acid sequence of the light chain variable region of A10K (SEQ ID NO: 6).

Figure 4A shows the amino acid sequence of the heavy chain variable region of A10K (SEQ ID NO: 7), and Figure 4B shows the nucleic acid sequence of the heavy chain variable region of A10K (SEQ ID NO: 8).

25 Figure 5A shows the amino acid sequence of a fully human light chain framework region with interspersed CDRs. The four framework sub-regions are labeled as follows: FRL1 (SEQ ID NO: 57), FRL2 (SEQ ID NO: 58), FRL3 (SEQ ID NO: 59), and FRL4 (SEQ ID NO: 60). Figure 5B shows the nucleic acid sequence of a fully human light chain framework region with interspersed CDRs. The four framework sub-regions are labeled as
30 follows: FRL1 (SEQ ID NO: 61), FRL2 (SEQ ID NO: 62), FRL3 (SEQ ID NO: 63), and FRL4 (SEQ ID NO: 64).

Figure 6A shows the amino acid sequence of a fully human heavy chain framework region with interspersed CDRs. The four framework sub-regions are labeled as follows: FRH1 (SEQ ID NO: 65), FRH2 (SEQ ID NO: 66), FRH3 (SEQ ID NO: 67), and FRH4

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(SEQ ID NO: 68). Figure 6B shows the nucleic acid sequence of a fully human heavy chain framework region with interspersed CDRs. The four framework sub-regions are labeled as follows: FRH1 (SEQ ID NO: 69), FRH2 (SEQ ID NO: 70), FRH3 (SEQ ID NO: 71), and FRH4 (SEQ ID NO: 72).

5   Figure 7 shows the results of an ELISA described in Example 1.

Figure 8 shows the results of an L929 cell protection assay described in Example 2.

Figure 9 shows the results of an L929 cell protection assay described in Example 2.

Figure 10 shows the results of an L929 cell protection assay described in Example 2.

Figure 11 shows the results of an in vivo TNF-α neutralizing assay described in

10   Example 3.

Figure 12 shows the effect of a TNF-α binding molecule in reducing progression of TNF-α mediated polyarthritis in mice, as described in Example 3.

Figure 13 shows a schematic representation of an IgG molecule with the various regions and sections labeled. The CDRs and framework regions (FR) of one of the two

15   variable region light chains, and one of the two variable region heavy chains, are also labeled.

Figure 14 shows the nucleic acid sequence of a human CL sequence, and a human CH1 sequence, that were used in the construction of the Fab fragments described in Example 1.

20   Figure 15 shows the complete light and heavy chain amino acid sequences for AME 3-2, the CDRs shown in bold.

DEFINITIONS

25   To facilitate an understanding of the invention, a number of terms are defined below.

The term "antibody," as used herein, is intended to refer to immunoglobulin molecules comprised of four polypeptide chains, two heavy (H) chains and two light (L) chains inter-connected by disulfide bonds. Each heavy chain is comprised of a heavy chain variable region (abbreviated herein as HCVR or VH) and a heavy chain constant region.

30   The heavy chain constant region is comprised of three domains, CH1, CH2 and CH3 (see Figure 13). Each light chain is comprised of a light chain variable region (abbreviated herein as LCVR or VL) and a light chain constant region. The light chain constant region is comprised of one domain, CL (see Figure 13). The VH and VL regions can be further subdivided into regions of hypervariability, termed complementarity determining regions

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(CDRs), interspersed with regions that are more conserved, termed framework regions (FR). Each variable region (VH or VL) contains 3 CDRs, designated CDR1, CDR2 and CDR3 (see Figures 5, 6, and 13). Each variable region also contains 4 framework sub-regions, designated FR1, FR2, FR3 and FR4 (see Figures 5, 6, and 13).

5   As used herein, the term "antibody fragments" refers to a portion of an intact antibody. Examples of antibody fragments include, but are not limited to, linear antibodies, single-chain antibody molecules, Fab and F(ab')$_2$ fragments, and multispecific antibodies formed from antibody fragments. The antibody fragments preferably retain at least part of the heavy and/or light chain variable region.

10   As used herein, the terms "complementarity determining region" and "CDR" refer to the regions that are primarily responsible for antigen-binding. There are three CDRs in a light chain variable region (CDRL1, CDRL2, and CDRL3), and three CDRs in a heavy chain variable region (CDRH1, CDRH2, and CDRH3). The residues that make up these six CDRs have been characterized by Kabat and Chothia as follows: residues 24-34 (CDRL1),

15   50-56 (CDRL2) and 89-97 (CDRL3) in the light chain variable region and 31-35 (CDRH1), 50-65 (CDRH2) and 95-102 (CDRH3) in the heavy chain variable region; Kabat et al., (1991) Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD., herein incorporated by reference; and residues 26-32 (CDRL1), 50-52 (CDRL2) and 91-96 (CDRL3) in the light chain variable region and

20   26-32 (CDRH1), 53-55 (CDRH2) and 96-101 (CDRH3) in the heavy chain variable region; Chothia and Lesk (1987) J. Mol. Biol. 196: 901-917, herein incorporated by reference. Unless otherwise specified, the terms "complementarity determining region" and "CDR" as used herein, include the residues that encompass both the Kabat and Chothia definitions (i.e., residues 24-34 (CDRL1), 50-56 (CDRL2), and 89-97 (CDRL3) in the light chain

25   variable region; and 26-35 (CDRH1), 50-65 (CDRH2), and 95-102 (CDRH3)). Also, unless specified, as used herein, the numbering of CDR residues is according to Kabat.

As used herein, the term "framework" refers to the residues of the variable region other than the CDR residues as defined herein. There are four separate framework sub-regions that make up the framework: FR1, FR2, FR3, and FR4 (See Figures 5, 6, and 13).

30   In order to indicate if the framework sub-region is in the light or heavy chain variable region, an "L" or "H" may be added to the sub-region abbreviation (e.g., "FRL1" indicates framework sub-region 1 of the light chain variable region). Unless specified, the numbering of framework residues is according to Kabat.

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As used herein, the term "fully human framework" means a framework with an amino acid sequence found naturally in humans. Examples of fully human frameworks, include, but are not limited to, KOL, NEWM, REI, EU, TUR, TEI, LAY and POM (See, e.g., Kabat et al., (1991) Sequences of Proteins of Immunological Interest, US Department

5   of Health and Human Services, NIH, USA; and Wu et al., (1970) J. Exp. Med. 132, 211-250, both of which are herein incorporated by reference).

As used herein, the terms "subject" and "patient" refer to any animal, such as a mammal like a dog, cat, bird, livestock, and preferably a human (e.g., a human with a TNF-α mediated disease).

10   As used herein, the terms "nucleic acid sequence encoding," "DNA sequence encoding," and "DNA encoding" refer to the order or sequence of deoxyribonucleotides along a strand of deoxyribonucleic acid. The order of these deoxyribonucleotides determines the order of amino acids along the polypeptide (protein) chain. The DNA sequence thus codes for the amino acid sequence.

15   DNA molecules are said to have "5' ends" and "3' ends" because mononucleotides are reacted to make oligonucleotides or polynucleotides in a manner such that the 5' phosphate of one mononucleotide pentose ring is attached to the 3' oxygen of its neighbor in one direction via a phosphodiester linkage. Therefore, an end of an oligonucleotide or polynucleotide, is referred to as the "5' end" if its 5' phosphate is not linked to the 3' oxygen

20   of a mononucleotide pentose ring and as the "3' end" if its 3' oxygen is not linked to a 5' phosphate of a subsequent mononucleotide pentose ring. As used herein, a nucleic acid sequence, even if internal to a larger oligonucleotide or polynucleotide, also may be said to have 5' and 3' ends. In either a linear or circular DNA molecule, discrete elements are referred to as being "upstream" or 5' of the "downstream" or 3' elements. This terminology

25   reflects the fact that transcription proceeds in a 5' to 3' fashion along the DNA strand. The promoter and enhancer elements that direct transcription of a linked gene are generally located 5' or upstream of the coding region. However, enhancer elements can exert their effect even when located 3' of the promoter element and the coding region. Transcription termination and polyadenylation signals are located 3' or downstream of the coding region.

30   As used herein, the term "codon" or "triplet" refers to a group of three adjacent nucleotide monomers which specify one of the naturally occurring amino acids found in polypeptides. The term also includes codons which do not specify any amino acid.

As used herein, the terms "an oligonucleotide having a nucleotide sequence encoding a polypeptide," "polynucleotide having a nucleotide sequence encoding a

polypeptide," and "nucleic acid sequence encoding a peptide" means a nucleic acid sequence comprising the coding region of a particular polypeptide. The coding region may be present in a cDNA, genomic DNA, or RNA form. When present in a DNA form, the oligonucleotide or polynucleotide may be single-stranded (i.e., the sense strand) or double-

5   stranded. Suitable control elements such as enhancers/promoters, splice junctions, polyadenylation signals, etc. may be placed in close proximity to the coding region of the gene if needed to permit proper initiation of transcription and/or correct processing of the primary RNA transcript. Alternatively, the coding region utilized in the expression vectors of the present invention may contain endogenous enhancers/promoters, splice junctions,

10   intervening sequences, polyadenylation signals, etc., or a combination of both endogenous and exogenous control elements.

Also, as used herein, there is no size limit or size distinction between the terms "oligonucleotide" and "polynucleotide." Both terms simply refer to molecules composed of nucleotides. Likewise, there is no size distinction between the terms "peptide" and

15   "polypeptide." Both terms simply refer to molecules composed of amino acid residues.

As used herein, the terms "complementary" or "complementarity" are used in reference to polynucleotides (i.e., a sequence of nucleotides) related by the base-pairing rules. For example, the sequence "5'-A-G-T 3", is complementary to the sequence "3-T-C-A-5'". Complementarity may be "partial", in which only some of the nucleic acids' bases

20   are matched according to the base pairing rules, or, there may be "complete" or "total" complementarity between the nucleic acids. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization. This is of particular importance in amplification reactions, as well as in detection methods that depend upon binding between nucleic acids.

25   As used herein, the term "the complement of" a given sequence is used in reference to the sequence that is completely complementary to the sequence over its entire length. For example, the sequence 5'-A-G-T-A-3' is "the complement" of the sequence 3'-T-C-A-T-5'. The present invention also provides the complement of the sequences described herein (e.g., the complement of the nucleic acid sequences in SEQ ID NOs: 1-84).

30   The term "homology" (when in reference to nucleic acid sequences) refers to a degree of complementarity. There may be partial homology or complete homology (i.e., identity). A partially complementary sequence is one that at least partially inhibits a completely complementary sequence from hybridizing to a target nucleic acid and is referred to using the functional term "substantially homologous".

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The term "inhibition of binding", when used in reference to nucleic acid binding, refers to inhibition of binding caused by competition of homologous sequences for binding to a target sequence. The inhibition of hybridization of the completely complementary sequence to the target sequence may be examined using a hybridization assay (Southern or

5   Northern blot, solution hybridization and the like) under conditions of low stringency. A substantially homologous sequence or probe will compete for and inhibit the binding (i.e., the hybridization) of a completely homologous sequence to a target under conditions of low stringency. This is not to say that conditions of low stringency are such that non-specific binding is permitted; low stringency conditions require that the binding of two sequences to

10   one another be a specific (i.e., selective) interaction. The absence of non-specific binding may be tested by the use of a second target that lacks even a partial degree of complementarity (e.g., less than about 30% identity); in the absence of non-specific binding the probe will not hybridize to the second non-complementary target.

The art knows well that numerous equivalent conditions may be employed to

15   comprise low stringency conditions; factors such as the length and nature (DNA, RNA, base composition) of the probe and the length and nature of the target (DNA, RNA, base composition, present in solution or immobilized, etc.) and the concentration of the salts and other components (e.g., the presence or absence of formamide, dextran sulfate, polyethylene glycol) are considered and the hybridization solution may be varied to generate conditions

20   of low stringency hybridization different from, but equivalent to, the above listed conditions. In addition, the art knows conditions that promote hybridization under conditions of high stringency (e.g., increasing the temperature of the hybridization and/or wash steps, the use of formamide in the hybridization solution, etc.).

As used herein, the term "hybridization" is used in reference to the pairing of

25   complementary nucleic acids. Hybridization and the strength of hybridization (i.e., the strength of the association between the nucleic acids) is impacted by such factors as the degree of complementarity between the nucleic acids, stringency of the conditions involved, the T_m of the formed hybrid, and the G:C ratio within the nucleic acids.

As used herein the term "stringency" is used in reference to the conditions of

30   temperature, ionic strength, and the presence of other compounds such as organic solvents, under which nucleic acid hybridizations are conducted. Those skilled in the art will recognize that "stringency" conditions may be altered by varying the parameters just described either individually or in concert. With "high stringency" conditions, nucleic acid base pairing will occur only between nucleic acid fragments that have a high frequency of

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complementary base sequences (e.g., hybridization under "high stringency" conditions may occur between homologs with about 85-100% identity, preferably about 70-100% identity). With medium stringency conditions, nucleic acid base pairing will occur between nucleic acids with an intermediate frequency of complementary base sequences (e.g., hybridization

5 under "medium stringency" conditions may occur between homologs with about 50-70% identity). Thus, conditions of "weak" or "low" stringency are often required with nucleic acids that are derived from organisms that are genetically diverse, as the frequency of complementary sequences is usually less.

"High stringency conditions" when used in reference to nucleic acid hybridization

10 comprise conditions equivalent to binding or hybridization at 42 C in a solution consisting of 5X SSPE (43.8 g/l NaCl, 6.9 g/l $NaH_2PO_4 H_2O$ and 1.85 g/l EDTA, pH adjusted to 7.4 with NaOH), 0.5% SDS, 5X Denhardt's reagent [50X Denhardt's contains per 500 ml: 5 g Ficoll (Type 400, Pharmacia), 5 g BSA (Fraction V; Sigma)] and 100 µg/ml denatured salmon sperm DNA, followed by washing in a solution comprising 0.1X SSPE, 1.0% SDS

15 at 42 C when a probe of about 500 nucleotides in length is employed.

"Medium stringency conditions" when used in reference to nucleic acid hybridization comprise conditions equivalent to binding or hybridization at 42°C in a solution consisting of 5X SSPE, 0.5% SDS, 5X Denhardt's reagent and 100 µg/ml denatured salmon sperm DNA, followed by washing in a solution comprising 1.0X SSPE,

20 1.0% SDS at 42 C when a probe of about 500 nucleotides in length is employed.

"Low stringency conditions" comprise conditions equivalent to binding or hybridization at 42 C in a solution consisting of 5X SSPE, 0.1% SDS, 5X Denhardt's reagent and 100 g/ml denatured salmon sperm DNA, followed by washing in a solution comprising 5X SSPE, 0.1% SDS at 42 C when a probe of about 500 nucleotides in length is

25 employed.

As used herein, the term "polymerase chain reaction" ("PCR") refers to the method described in U.S. Patent Nos. 4,683,195, 4,683,202, and 4,965,188, hereby incorporated by reference, that describe a method for increasing the concentration of a segment of a target sequence in a mixture of genomic DNA without cloning or purification. This process for

30 amplifying the target sequence consists of introducing a large excess of two oligonucleotide primers to the DNA mixture containing the desired target sequence, followed by a precise sequence of thermal cycling in the presence of a DNA polymerase. The two primers are complementary to their respective strands of the double stranded target sequence. To effect amplification, the mixture is denatured and the primers then annealed to their

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complementary sequences within the target molecule. Following annealing, the primers are extended with a polymerase so as to form a new pair of complementary strands. The steps of denaturation, primer annealing, and polymerase extension can be repeated many times (i.e., denaturation, annealing and extension constitute one "cycle"; there can be numerous

5   "cycles") to obtain a high concentration of an amplified segment of the desired target sequence. The length of the amplified segment of the desired target sequence is determined by the relative positions of the primers with respect to each other, and therefore, this length is a controllable parameter. By virtue of the repetitive aspect of the process, the method is referred to as the "polymerase chain reaction" (hereinafter "PCR"). Because the desired

10   amplified segments of the target sequence become the predominant sequences (in terms of concentration) in the mixture, they are said to be "PCR amplified".

   With PCR, it is possible to amplify a single copy of a specific target sequence in genomic DNA to a level detectable by several different methodologies (e.g., hybridization with a labeled probe; incorporation of biotinylated primers followed by avidin-enzyme

15   conjugate detection; incorporation of ^{32}P-labeled deoxynucleotide triphosphates, such as dCTP or dATP, into the amplified segment). In addition to genomic DNA, any oligonucleotide or polynucleotide sequence can be amplified with the appropriate set of primer molecules. In particular, the amplified segments created by the PCR process are, themselves, efficient templates for subsequent PCR amplifications.

20   The term "isolated" when used in relation to a nucleic acid, as in "an isolated oligonucleotide" or "isolated polynucleotide" or "isolated nucleic acid sequence encoding a TNF-α binding molecule" refers to a nucleic acid sequence that is identified and separated from at least one contaminant nucleic acid with which it is ordinarily associated in its natural source. Isolated nucleic acid is present in a form or setting that is different from that

25   in which it is found in nature. Isolated nucleic acid molecules therefore are distinguished from the nucleic acid molecule as it exists in natural cells. However, an isolated nucleic acid molecule includes a nucleic acid molecule contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells. The isolated nucleic acid, oligonucleotide, or

30   polynucleotide may be present in single-stranded or double-stranded form. When an isolated nucleic acid, oligonucleotide or polynucleotide is to be utilized to express a protein, the oligonucleotide or polynucleotide will contain at a minimum the sense or coding strand (i.e., the oligonucleotide or polynucleotide may be single-stranded), but may contain both

the sense and anti-sense strands (i.e., the oligonucleotide or polynucleotide may be double-stranded).

As used herein, the terms "portion" when used in reference to a nucleotide sequence (as in "a portion of a given nucleotide sequence") refers to fragments of that sequence. The

5   fragments may range in size from ten nucleotides to the entire nucleotide sequence minus one nucleotide (e.g., 10 nucleotides, 20, 30, 40, 50, 100, 200, etc.).

As used herein, the term "portion" when in reference to an amino acid sequence (as in "a portion of a given amino acid sequence") refers to fragments of that sequence. The fragments may range in size from six amino acids to the entire amino acid sequence minus

10   one amino acid (e.g., 6 amino acids, 10, 20, 30, 40, 75, 200, etc.).

As used herein, the term "purified" or "to purify" refers to the removal of contaminants from a sample. For example, TNF-α specific antibodies may be purified by removal of contaminating non-immunoglobulin proteins; they are also purified by the removal of immunoglobulins that do not bind to the same antigen. The removal of non-

15   immunoglobulin proteins and/or the removal of immunoglobulins that do not bind the particular antigen results in an increase in the percentage of antigen specific immunoglobulins in the sample. In another example, recombinant antigen-specific polypeptides are expressed in bacterial host cells and the polypeptides are purified by the removal of host cell proteins; the percentage of recombinant antigen-specific polypeptides is

20   thereby increased in the sample.

The term "recombinant DNA molecule" as used herein refers to a DNA molecule that is comprised of segments of DNA joined together by means of molecular biological techniques.

The term "recombinant protein" or "recombinant polypeptide" as used herein refers

25   to a protein molecule that is expressed from a recombinant DNA molecule.

As used herein, the term "vector" is used in reference to nucleic acid molecules that transfer DNA segment(s) from one cell to another. The term "vehicle" is sometimes used interchangeably with "vector."

The term "expression vector" as used herein refers to a recombinant DNA molecule

30   containing a desired coding sequence and appropriate nucleic acid sequences necessary for the expression of the operably linked coding sequence in a particular host organism. Nucleic acid sequences necessary for expression in prokaryotes usually include a promoter, an operator (optional), and a ribosome binding site, often along with other sequences.

25

Eukaryotic cells are known to utilize promoters, enhancers, and termination and
polyadenylation signals.

As used herein, the term "host cell" refers to any eukaryotic or prokaryotic cell (e.g.,
bacterial cells such as *E. coli*, yeast cells, mammalian cells such as PER.C6™ (Crucell, The
5   Netherlands) and CHO cells, avian cells, amphibian cells, plant cells, fish cells, and insect
cells), whether located in vitro or in vivo. For example, host cells may be located in a
transgenic animal.

The terms "transfection" and "transformation" as used herein refer to the
introduction of foreign DNA into cells (e.g., eukaryotic and prokaryotic cells). Transfection
10   may be accomplished by a variety of means known to the art including calcium phosphate-
DNA co-precipitation, DEAE-dextran-mediated transfection, polybrene-mediated
transfection, electroporation, microinjection, liposome fusion, lipofection, protoplast fusion,
retroviral infection, and biolistics.

The term "stable transfection" or "stably transfected" refers to the introduction and
15   integration of foreign DNA into the genome of the transfected cell. The term "stable
transfectant" refers to a cell that has stably integrated foreign DNA into the genomic DNA.

The term "transient transfection" or "transiently transfected" refers to the
introduction of foreign DNA into a cell where the foreign DNA fails to integrate into the
genome of the transfected cell. The foreign DNA persists in the nucleus of the transfected
20   cell for several days. During this time, the foreign DNA is subject to the regulatory controls
that govern the expression of endogenous genes in the chromosomes. The term "transient
transfectant" refers to cells that have taken up foreign DNA but have failed to integrate this
DNA.

As used herein, the terms "computer memory" and "computer memory device" refer
25   to any storage media readable by a computer processor. Examples of computer memory
include, but are not limited to, RAM, ROM, computer chips, digital video discs (DVDs),
compact discs (CDs), hard disk drives (HDD), and magnetic tapes.

As used herein, the term "computer readable medium" refers to any device or system
for storing and providing information (e.g., data and instructions) to a computer processor.
30   Examples of computer readable media include, but are not limited to, DVDs, CDs, hard disk
drives, magnetic tapes and servers for streaming media over networks.

As used herein, the phrase "computer readable medium encodes a representation" of
a nucleic acid or amino acid sequence, refers to computer readable medium that has stored

thereon information, that when delivered to a processor, allows the nucleic or amino acid sequence to be displayed to a user (e.g., printed out or presented on a display screen).

As used herein, the terms "processor" and "central processing unit" or "CPU" are used interchangeably and refer to a device that is able to read a program from a computer memory (e.g., ROM or other computer memory) and perform a set of steps according to the program.

As used herein, the term "Fc region" refers to a C-terminal region of an immunoglobulin heavy chain (e.g., as shown in Figure 13). The "Fc region" may be a native sequence Fc region or a variant Fc region (e.g., with increased or decreased effector functions).

As used herein, an Fc region may possess "effector functions" that are responsible for activating or diminishing a biological activity (e.g., in a subject). Examples of effector functions include, but are not limited to: C1q binding; complement dependent cytotoxicity (CDC); Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (e.g., B cell receptor; BCR), etc. Such effector functions may require the Fc region to be combined with a binding domain (e.g., an antibody variable domain) and can be assessed using various assays (e.g. Fc binding assays, ADCC assays, CDC assays, etc.).

As used herein, an "isolated" peptide, polypeptide, or protein is one that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In certain embodiments, the isolated polypeptide is purified (1) to greater than 95% by weight of polypeptides as determined by the Lowry method, and preferably, more than 99% by weight; (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-page under reducing or nonreducing conditions using Coomassie blue, or silver stain. An isolated polypeptide includes the polypeptide in situ within recombinant cells since at least one component of the polypeptide's natural environment will not be present. Ordinarily, however, an isolated polypeptide will be prepared by a least one purification step.

As used herein, the term "treatment" refers to both therapeutic treatment and prophylactic or preventative measures. Those in need of treatment include those already with the disorder as well as those in which the disorder is to be prevented.

As used herein, nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is

5   operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. In preferred embodiments, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading frame. However, enhancers, for example, do not have to be contiguous. Linking

10 may be accomplished, for example, by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers may be used in accordance with conventional practice.

The phrase "under conditions such that the symptoms are reduced" refers to any degree of qualitative or quantitative reduction in detectable symptoms of any TNF-α

15 mediated disease, including but not limited to, a detectable impact on the rate of recovery from disease (e.g., rate of weight gain), or the reduction of at least one of the symptoms normally associated with the particular disease (e.g., if the TNF-α mediated disease were Crohn's disease, a reduction in at least one of the following symptoms: abdominal pain, diarrhea, rectal bleeding, weight loss, fever, loss of appetite, dehydration, anemia,

20 distention, fibrosis, inflamed intestines and malnutrition).

The term "human TNF-α" (abbreviated herein as hTNF-α, or simply hTNF), as used herein, is intended to refer to a human cytokine that exists as a 17 kDa secreted form and a 26 kDa membrane associated form, the biologically active form of which is composed of a trimer of noncovalently bound 17 kDa molecules. The structure of hTNF-α is described

25 further in, for example, Jones, et al. (1989) Nature, 338:225-228. The term human TNF-α is intended to include recombinant human TNF-α (rhTNF-α), which can be prepared by standard recombinant expression methods or purchased commercially.

The terms "affinity", "binding affinity" and "K_d" refer to the equilibrium dissociation constant (expressed in units of concentration) associated with each TNF-α binding molecule

30 – TNF-α protein complex. The binding affinity is directly related to the ratio of the off-rate constant (generally reported in units of inverse time, e.g., seconds^{-1}) to the on-rate constant (generally reported in units of concentration per unit time, e.g., molar/second). The binding affinity may be determined by, for example, a kinetic exclusion assay or surface plasmon resonance.

28

The terms "dissociation", "dissociation rate" and "k_{off}" as used herein, are intended to refer to the off rate constant for dissociation of a TNF-α binding molecule from the antibody/antigen complex.

The terms "association", "association rate" and "k_{on}" as used herein, are intended to refer to the on rate constant for association of a TNF-α binding molecule with an antigen to form an antibody/antigen complex.

The terms "effective concentration" and "EC_{50}" as used herein, are intended to refer to the concentration of a TNF-α binding molecule capable of interacting with, and neutralizing sufficient quantities of TNF-α molecules to produce an effect on approximately 50% of the treated cells. For example, in an L929 assay (See Example 2), the EC_{50} is the concentration necessary to protect approximately 50% of the cells from TNF-α mediated cytotoxicity. In these assays, the concentration of TNF-α used is empirically determined in order to exert a cytotoxic effect on ≥ than 90% of the cell population. Also, herein, no distinction is made between effective (EC_{50}) and inhibitory (IC_{50}) concentration.

DESCRIPTION OF THE INVENTION

The present invention provides TNF-α binding molecules and nucleic acid sequences encoding TNF-α binding molecules. In particular, the present invention provides TNF-α binding molecules with a high binding affinity, a high association rate, a low dissociation rate with regard to human TNF-α and a low EC_{50} value (e.g., in an L929 cell assay). Preferably, the TNF-α binding molecules of the present invention comprise light and/or heavy chain variable regions with fully human frameworks. In particularly preferred embodiments, the TNF-α binding molecules of the present invention comprise light and/or heavy chain variable regions with human germline frameworks. The description of the invention is divided into the following sections below for convenience: I. TNF-α Binding Molecules; II. Generating TNF-α Binding Molecules; III. Therapeutic Formulations and Uses; and IV. Additional TNF-α Binding Molecule Uses.

I.   TNF-α Binding Molecules

The present invention provides TNF-α binding molecules with desirable characteristics. In particular, in some embodiments, the TNF-α binding molecules have a high binding affinity (K_d) with regard to human TNF-α. In other embodiments, the TNF-α binding molecules have a high association rate constant (k_{on}) with regard to human TNF-α.

In certain embodiments, the TNF-α binding molecules have a low dissociation rate (k_{off}) with regard to human TNF-α. In other embodiments, the TNF-α binding molecules have a low effective concentration (EC_{50}) in cell-based assays. In preferred embodiments, the TNF-α binding molecules of the present invention have a high binding affinity, a high

5   association rate, a low dissociation rate and are effective at a low concentrations. While not necessary to practice or understand the invention, it is believed that the TNF-α binding molecules of the present invention, with high binding affinity, a high association rate, a low dissociation rate and a low EC_{50}, are particularly well suited for therapeutic use in humans (e.g., for treating TNF-α mediated diseases).

10   In further embodiments, the TNF-α binding molecules of the present invention do not bind murine TNF-α. In other embodiments, the TNF-α binding molecules of the present invention do not bind rat, pig, or rhesus macaque TNF-α.

      In preferred embodiments, the TNF-α binding molecules of the present invention comprise a light and/or heavy chain variable region, preferably having a fully human framework. In particularly preferred embodiments, the TNF-α binding molecules of the

15   present invention comprise a light and/or heavy chain variable region, preferably having a human germline framework. While not necessary to practice or understand the invention, it is believed that the TNF-α binding molecules of the present invention (see, e.g. the Examples below) will illicit very little or no immunogenic response when administered to a

20   human (e.g. to treat a disease).

      As described below in Tables 1, 2, 3, and 6 the present invention provides numerous CDRs useful for generating TNF-α binding molecules. For example, one or more of the CDRs shown can be combined with a framework sub-region (e.g., a fully human FR1, FR2, FR3, or FR4) in order to generate a TNF-α binding peptide, or a nucleic acid sequence

25   encoding a TNF-α binding peptide. Also, the CDRs shown in the Tables below may be combined, for example, such that three CDRs are present in a light chain variable region, and/or three CDRs are present in a heavy chain variable region.

      The CDRs shown below may be inserted into a human framework (by recombinant techniques) into the light and heavy chain frameworks shown in Figures 5 and 6 in order to

30   generate TNF-α binding molecules or nucleic acid sequences encoding TNF-α binding molecules. For example, the CDRL1 shown in Figure 5A could be replaced by SEQ ID NO: 9, 11, 13, 15, or 17 as shown in Table 1. Likewise, the CDRL1 shown in Figure 5B could be replaced by SEQ ID NO: 10, 12, 14, 16, or 18 and shown in Table 1. This same

procedure may be used with all of the CDRs shown in Tables 1-3 and 6. These three tables are show immediately below.

TABLE 1 - Light Chain CDRs

SEQ ID NO	CDR Name*	change from hu1**	Sequence ***
SEQ ID NO:9	CDRL1	none	RASQFVGSSIH
SEQ ID NO:10	CDRL1	none	AGGGCCAGTCAGTTCGTTGGCTCAAGCATCCAC
SEQ ID NO:11	CDRL1	S31L	RASQFVGLSIH
SEQ ID NO:12	CDRL1	S31L	AGGGCCAGTCAGTTCGTTGGCCTTAGCATCCAC
SEQ ID NO:13	CDRL1	S31M	RASQFVGMSIH
SEQ ID NO:14	CDRL1	S31M	AGGGCCAGTCAGTTCGTTGGCATGAGCATCCAC
SEQ ID NO:15	CDRL1	S31Y	RASQFVGYSIH
SEQ ID NO:16	CDRL1	S31Y	AGGGCCAGTCAGTTCGTTGGCTATAGCATCCAC
SEQ ID NO:17	CDRL1	S31Xaa	RASQFVGXaaSIH
SEQ ID NO:18	CDRL1	S31Xaa	AGGGCCAGTCAGTTCGTTGGCnnnAGCATCCAC
SEQ ID NO:19	CDRL2	none	YASESMS
SEQ ID NO:20	CDRL2	none	TATGCTTCTGAGTCTATGTCT
SEQ ID NO:21	CDRL2	S54Y	YASEYMS
SEQ ID NO:22	CDRL2	S54Y	TATGCTTCTGAGTATATGTCT
SEQ ID NO:23	CDRL2	S54Xaa	YASEXaaMS
SEQ ID NO:24	CDRL2	S54Xaa	TATGCTTCTGAGnnnATGTCT
SEQ ID NO:25	CDRL2	M55R	YASESRS
SEQ ID NO:26	CDRL2	M55R	TATGCTTCTGAGTCTAGGTCT
SEQ ID NO:27	CDRL2	M55K	YASESKS
SEQ ID NO:28	CDRL2	M55K	TATGCTTCTGAGTCTAAGTCT
SEQ ID NO:29	CDRL2	M55Xaa	YASESXaaS
SEQ ID NO:30	CDRL2	M55Xaa	TATGCTTCTGAGTCTnnnTCT
SEQ ID NO:31	CDRL2	S54Xaa and M55Xaa	YASEXaaXaaS
SEQ ID NO:32	CDRL2	S54Xaa and M55Xaa	TATGCTTCTGAGnnnnnnTCT
SEQ ID NO:33	CDRL3	none	QQSHSWHFT
SEQ ID NO:34	CDRL3	none	CAACAAAGTCATAGCTGGCATTTCACG

5

*The work of Kabat was used to number residues. CDRs include Kabat and Chothia residues.

** Changes from hu1 are designated by the hu1 amino acid, followed by the position, and then the new amino acid (e.g., S31L is a change from S at position 31 to L).

***"Xaa" indicates this position can be any amino acid, and "n" indicates this position can be any nucleotide.

5

TABLE 2 - Heavy Chain CDRs

SEQ ID NO	CDR Name*	change from hu1**	Sequence***
SEQ ID NO:35	CDRH1	none	GFTFSNHWMN
SEQ ID NO:36	CDRH1	none	GGATTCACTTTCAGTAACCACTGGATGAAC
SEQ ID NO:37	CDRH1	T28K	GFKFSNHWMN
SEQ ID NO:38	CDRH1	T28K	GGATTCAAGTTCAGTAACCACTGGATGAAC
SEQ ID NO:39	CDRH1	T28P	GFPFSNHWMN
SEQ ID NO:40	CDRH1	T28P	GGATTCCCTTTCAGTAACCACTGGATGAAC
SEQ ID NO:41	CDRH1	T28Xaa	GFXaaFSNHWMN
SEQ ID NO:42	CDRH1	T28Xaa	GGATTCnnnTTCAGTAACCACTGGATGAAC
SEQ ID NO:43	CDRH2	none	EIRSKSINSATHYAESVKG
SEQ ID NO:44	CDRH2	none	GAAATTAGATCAAAATCTATTAATTCTGCAACACATTATGCGGAGTCTGTGAAAGGG
SEQ ID NO:45	CDRH2	I53M	EIRSKSMNSATHYAESVKG
SEQ ID NO:46	CDRH2	I53M	GAAATTAGATCAAAATCTATGAATTCTGCAACACATTATGCGGAGTCTGTGAAAGGG
SEQ ID NO:47	CDRH2	I53Xaa	EIRSKSXaaNSATHYAESVKG
SEQ ID NO:48	CDRH2	I53Xaa	GAAATTAGATCAAAATCTnnnAATTCTGCAACACATTATGCGGAGTCTGTGAAAGGG
SEQ ID NO:49	CDRH2	E61R	EIRSKSINSATHYARSVKG
SEQ ID NO:50	CDRH2	E61R	GAAATTAGATCAAAATCTATTAATTCTGCAACACATTATGCGCGTTCTGTGAAAGGG
SEQ ID NO:51	CDRH2	E61Xaa	EIRSKSINSATHYAXaaSVKG
SEQ ID NO:52	CDRH2	E61Xaa	GAAATTAGATCAAAATCTATTAATTCTGCAACACATTATGCGnnnTCTGTGAAAGGG
SEQ ID NO:55	CDRH2	I53M + E61R	EIRSKSMNSATHYARSVKG
SEQ ID NO:56	CDRH2	I53M + E61R	GAAATTAGATCAAAATCTATGAATTCTGCAACACATTATGCGCGTTCTGTGAAAGGG
SEQ ID NO:53	CDRH3	none	NYYGSTYDH
SEQ ID NO:54	CDRH3	none	AATTACTACGGTAGTACCTACGACCAT

*The work of Kabat was used to number residues. CDRs include both Kabat and Chothia residues.

** Changes from hu1 are designated by the hu1 amino acid, followed by the position, and then the new amino acid (e.g., T28K is a change from T at position 28 to K).

***"Xaa" indicates this position can be any amino acid, and "n" indicates this position can be any nucleotide.

5   TABLE 3 - Additional beneficial CDRs

SEQ ID NO:73	CDRL1	S26P	RAPQFVGSSIH
SEQ ID NO:74	CDRL1	S26P	AGGGCCCCTCAGTTCGTTGGCTCAAGCATCCAC
SEQ ID NO:75	CDRL1	S26Xaa	RAXaaQFVGSSIH
SEQ ID NO:76	CDRL1	S26Xaa	AGGGCCnnnCAGTTCGTTGGCTCAAGCATCCAC
SEQ ID NO:77	CDRL1	G30Y	RASQFVYSSIH
SEQ ID NO:78	CDRL1	G30Y	AGGGCCAGTCAGTTCGTTTATTCAAGCATCCAC
SEQ ID NO:79	CDRL1	G30Xaa	RASQFVXaaSSIH
SEQ ID NO:80	CDRL1	G30Xaa	AGGGCCAGTCAGTTCGTTnnnTCAAGCATCCAC
SEQ ID NO:81	CDRL3	S93W	QQSHWWHFT
SEQ ID NO:82	CDRL3	S93W	CAACAAAGTCATTGGTGGCATTTCACG
SEQ ID NO:83	CDRL3	S93Xaa	QQSHXaaWHFT
SEQ ID NO:84	CDRL3	S93Xaa	CAACAAAGTCATnnnTGGCATTTCACG

*The work of Kabat was used to number residues. CDRs include both Kabat and Chothia residues.

** Changes from hu1 are designated by the hu1 amino acid, followed by the position, and then the new amino acid (e.g., T28K is a change from T at position 28 to K)

10   ***"Xaa" indicates this position can be any amino acid, and "n" indicates this position can be any nucleotide.

                           TABLE 6 - Additional beneficial CDRs

SEQ ID NO:87	CDRH1	GFTFRNHWMN
SEQ ID NO:88	CDRH1	GGATTCACTTTCCGGAACCACTGGATGAAC
SEQ ID NO:89	CDRH2	EIRSKSINSATFYAESVKG
SEQ ID NO:90	CDRH2	GAAATTAGATCAAAATCTATTAATTCTGCAACATTTTATGCGGAGTCTGTGAAAGGG
SEQ ID NO:91	CDRH3	NYYGSYYDH
SEQ ID NO:92	CDRH3	AATTACTACGGTAGTTATTACGACCAT
SEQ ID NO:93	CDRL1	VTTQFVGYAIH
SEQ ID NO:94	CDRL1	GTTACTACTCAGTTCGTTGGCTATGCTATCCAC
SEQ ID NO:95	CDRL2	YASSSRS
SEQ ID NO:96	CDRL2	TATGCTTCTTCGTCTAGGTCT
SEQ ID NO:97	CDRL3	QQSHGWPFT
SEQ ID NO:98	CDRL3	CAACAAAGTCATGGGTGGCCTTTCACG

SEQ ID NO:99	CDRH1	GFKFRNHWMN
SEQ ID NO:100	CDRH1	GGATTCAAGTTCCGTAACCACTGGATGAAC
SEQ ID NO:101	CDRH1	GFDFRNHWMN
SEQ ID NO:102	CDRH1	GGATTCGATTTCCGGAACCACTGGATGAAC
SEQ ID NO:103	CDRH2	EIRSKSMNSATFYAESVKG
SEQ ID NO:104	CDRH2	GAAATTAGATCAAAATCTATGAATTCTGCAACATTTTATGCGGAGTC TGTGAAAGGG
SEQ ID NO:105	CDRL1	AASQFVGQAIH
SEQ ID NO:106	CDRL1	GCGGCTTCTCAGTTCGTTGGCCAGGCGATCCAC
SEQ ID NO:107	CDRL2	YANESRS
SEQ ID NO:108	CDRL2	TATGCTAATGAGTCTAGGTCT

*The work of Kabat was used to number residues. CDRs include both Kabat and Chothia residues.

The present invention also provides sequences that are substantially the same as the

5   CDR sequences (both amino acid and nucleic acid) shown in the above Tables For

example, one or two amino acid may be changed in the sequences shown in the Tables.

Also for example, a number of nucleotide bases may be changed in the sequences shown in

the Tables. Changes to the amino acid sequence may be generated by changing the nucleic

acid sequence encoding the amino acid sequence. A nucleic acid encoding a variant of a

10   given CDR may be prepared by methods known in the art using the guidance of the present

specification for particular sequences. These methods include, but are not limited to,

preparation by site-directed (or oligonucleotide-mediated) mutagenesis, PCR mutagenesis,

and cassette mutagenesis of an earlier prepared nucleic acid encoding the CDR. Site-

directed mutagenesis is a preferred method for preparing substitution variants. This

15   technique is well known in the art (see, e.g., Carter et al., (1985) Nucleic Acids Res. 13:

4431-4443 and Kunkel et. al., (1987) Proc. Natl. Acad. Sci. USA 82: 488-492, both of

which are hereby incorporated by reference).

Briefly, in carrying out site-directed mutagenesis of DNA, the starting DNA is

altered by first hybridizing an oligonucleotide encoding the desired mutation to a single

20   strand of such starting DNA. After hybridization, a DNA polymerase is used to synthesize

an entire second strand, using the hybridized oligonucleotide as a primer, and using the

single strand of the starting DNA as a template. Thus, the oligonucleotide encoding the

desired mutation is incorporated in the resulting double-stranded DNA.

PCR mutagenesis is also suitable for making amino acid sequence variants of the

25   starting CDR (see, e.g., Vallette et. al., (1989) Nucleic Acids Res. 17: 723-733, hereby

incorporated by reference). Briefly, when small amounts of template DNA are used as starting material in a PCR, primers that differ slightly in sequence from the corresponding region in a template DNA can be used to generate relatively large quantities of a specific DNA fragment that differs from the template sequence only at the positions where the

5   primers differ from the template.

Another method for preparing variants, cassette mutagenesis, is based on the technique described by Wells et al., (1985) Gene 34: 315-323, hereby incorporated by reference. The starting material is the plasmid (or other vector) comprising the starting CDR DNA to be mutated. The codon(s) in the starting DNA to be mutated are identified.

10 There should be a unique restriction endonuclease site on each side of the identified mutation site(s). If no such restriction sites exist, they may be generated using the above-described oligonucleotide-mediated mutagenesis method to introduce them at appropriate locations in the starting polypeptide DNA. The plasmid DNA is cut at these sites to linearize it. A double-stranded oligonucleotide encoding the sequence of the DNA between

15 the restriction sites but containing the desired mutation(s) is synthesized using standard procedures, wherein the two strands of the oligonucleotide are synthesized separately and then hybridized together using standard techniques. This double-stranded oligonucleotide is referred to as the cassette. This cassette is designed to have 5' and 3' ends that are compatible with the ends of the linearized plasmid, such that it can be directly ligated to the

20 plasmid. This plasmid now contains the mutated DNA sequence.

Alternatively, or additionally, the desired amino acid sequence encoding a polypeptide variant can be determined, and a nucleic acid sequence encoding such amino acid sequence variant can be generated synthetically. Conservative modifications in the amino acid sequences of the CDRs may also be made. Naturally occurring residues are

25 divided into classes based on common side-chain properties:

(1) hydrophobic: norleucine, met, ala, val, leu, ile;

(2) neutral hydrophilic: cys, ser, thr;

(3) acidic: asp, glu;

(4) basic: asn, gln, his, lys, arg;

30 (5) residues that influence chain orientation: gly, pro; and

(6) aromatic: trp, tyr, phe.

Conservative substitutions will entail exchanging a member of one of these classes for another member of the same class. The present invention also provides the complement of the nucleic acid sequences shown in Tables 1-3 and 6, as well as nucleic acid sequences that

will hybridize to these nucleic acid sequences under low, medium, and high stringency conditions.

The CDRs of the present invention may be employed with any type of framework. Preferably, the CDRs are used with fully human frameworks, or framework sub-regions. In

5   particularly preferred embodiments, the frameworks are human germline sequences. One example of a fully human framework is shown in Figures 5 and 6. Another example is shown in Figure 15. Other fully human frameworks or framework sub-regions may also be employed. For example, the NCBI web site contains the sequences for the currently known human framework regions. Examples of human VH sequences include, but are not limited

10   to, VH1-18, VH1-2, VH1-24, VH1-3, VH1-45, VH1-46, VH1-58, VH1-69, VH1-8, VH2-26, VH2-5, VH2-70, VH3-11, VH3-13, VH3-15, VH3-16, VH3-20, VH3-21, VH3-23, VH3-30, VH3-33, VH3-35, VH3-38, VH3-43, VH3-48, VH3-49, VH3-53, VH3-64, VH3-66, VH3-7, VH3-72, VH3-73, VH3-74, VH3-9, VH4-28, VH4-31, VH4-34, VH4-39, VH4-4, VH4-59, VH4-61, VH5-51, VH6-1, and VH7-81, which are provided in Matsuda et al.,

15   (1998) J. Exp. Med. 188:1973-1975, that includes the complete nucleotide sequence of the human immunoglobulin chain variable region locus, herein incorporated by reference. Examples of human VK sequences include, but are not limited to, A1, A10, A11, A14, A17, A18, A19, A2, A20, A23, A26, A27, A3, A30, A5, A7, B2, B3, L1, L10, L11, L12, L14, L15, L16, L18, L19, L2, L20, L22, L23, L24, L25, L4/18a, L5, L6, L8, L9, O1, O11, O12,

20   O14, O18, O2, O4, and O8, which are provided in Kawasaki et al., (2001) Eur. J. Immunol. 31:1017-1028; Schable and Zachau, (1993) Biol. Chem. Hoppe Seyler 374:1001-1022; and Brensing-Kuppers et al., (1997) Gene 191:173-181, all of which are herein incorporated by reference. Examples of human VL sequences include, but are not limited to, V1-11, V1-13, V1-16, V1-17, V1-18, V1-19, V1-2, V1-20, V1-22, V1-3, V1-4, V1-5, V1-7, V1-9, V2-1,

25   V2-11, V2-13, V2-14, V2-15, V2-17, V2-19, V2-6, V2-7, V2-8, V3-2, V3-3, V3-4, V4-1, V4-2, V4-3, V4-4, V4-6, V5-1, V5-2, V5-4, and V5-6, which are provided in Kawasaki et al., (1997) Genome Res. 7:250-261, herein incorporated by reference. Fully human frameworks can be selected from any of these functional germline genes. Generally, these frameworks differ from each other by a limited number of amino acid changes. These

30   frameworks may be used with the CDRs described herein. For example, L6, a frequently used gene among the Vk3 sub-family could be selected as an alternate framework for the light chain of the TNF-α binding molecules of the present invention. Additional examples of human frameworks which may be used with the CDRs of the present invention include, but are not limited to, KOL, NEWM, REI, EU, TUR, TEI, LAY and POM (See, e.g., Kabat

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et al., (1991) Sequences of Proteins of Immunological Interest, US Department of Health and Human Services, NIH, USA; and Wu et al., (1970), J. Exp. Med. 132:211-250, both of which are herein incorporated by reference).

5   Again, while not necessary to practice or understand the invention, it is believed that the reason the use of germline sequences is expected to help eliminate adverse immune responses in most individuals is as follows. Somatic mutations frequently occur in the variable region of immunoglobulins as a result of the affinity maturation step that takes place during a normal immune response. Although these mutations are predominantly clustered around the hypervariable CDRs, they also impact residues in the framework

10   regions. These framework mutations are not present in the germline genes and are likely to be immunogenic in patients. In contrast, the general population has been exposed to the vast majority of framework sequences expressed from germline genes and, as a result of immunologic tolerance, these germline frameworks are expected to be less, or non-immunogenic in patients. In order to maximize the likelihood of tolerance, genes encoding

15   the variable regions can be selected from a collection of commonly occurring, functional germline genes, and genes encoding VH and VL regions can be further selected to match known associations between specific heavy and light chains of immunoglobulin molecules.

II.   Generating TNF-α Binding Molecules

20   In preferred embodiments, the TNF-α binding molecules of the present invention comprise antibodies or antibody fragments (e.g., comprising one or more of the CDRs described herein). An antibody, or antibody fragment, of the present invention can be prepared by recombinant expression of immunoglobulin light and heavy chain genes in a host cell. For example, to express an antibody recombinantly, a host cell may be transfected

25   with one or more recombinant expression vectors carrying DNA fragments encoding the immunoglobulin light and heavy chains of the antibody such that the light and heavy chains are expressed in the host cell and, preferably, secreted into the medium in which the host cell is cultured, from which medium the antibody can be recovered. Standard recombinant DNA methodologies may be used to obtain antibody heavy and light chain genes,

30   incorporate these genes into recombinant expression vectors and introduce the vectors into host cells, such as those described in Sambrook, Fritsch and Maniatis (eds), Molecular Cloning; A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), Ausubel, F. M. et al. (eds.) Current Protocols in Molecular Biology, Greene Publishing

Associates, (1989) and in U.S. Pat. No. 4,816,397 by Boss et al., all of which are herein

incorporated by reference.

To express an antibody with one or more of the CDRs of the present invention,

DNA fragments encoding the light and heavy chain variable regions are first obtained.

5   These DNAs can be obtained by amplification and modification of germline light and heavy

chain variable sequences using the polymerase chain reaction (PCR). Germline DNA

sequences for human heavy and light chain variable region genes are known in the art (see

above).

Once the germline VH and VL fragments are obtained, these sequences can be

10   mutated to encode one or more of the CDR amino acid sequences disclosed herein (see, e.g.,

Tables 1-3 and 6). The amino acid sequences encoded by the germline VH and VL DNA

sequences may be compared to the CDRs sequence(s) desired to identify amino acid

residues that differ from the germline sequences. Then the appropriate nucleotides of the

germline DNA sequences are mutated such that the mutated germline sequence encodes the

15   selected CDRs (e.g., the six CDRs that are selected from Tables 1-3 and 6), using the

genetic code to determine which nucleotide changes should be made. Mutagenesis of the

germline sequences may be carried out by standard methods, such as PCR-mediated

mutagenesis (in which the mutated nucleotides are incorporated into the PCR primers such

that the PCR product contains the mutations) or site-directed mutagenesis. In other

20   embodiments, the variable region is synthesized de novo (e.g., using a nucleic acid

synthesizer).

Once DNA fragments encoding the desired VH and VL segments are obtained (e.g.,

by amplification and mutagenesis of germline VH and VL genes, or synthetic synthesis, as

described above), these DNA fragments can be further manipulated by standard

25   recombinant DNA techniques, for example to convert the variable region genes to full-

length antibody chain genes, to Fab fragment genes or to a scFv gene. In these

manipulations, a VL- or VH-encoding DNA fragment is operably linked to another DNA

fragment encoding another polypeptide, such as an antibody constant region or a flexible

linker. The isolated DNA encoding the VH region can be converted to a full-length heavy

30   chain gene by operably linking the VH-encoding DNA to another DNA molecule encoding

heavy chain constant regions (CH1, CH2 and CH3). The sequences of human heavy chain

constant region genes are known in the art (see e.g., Kabat, E. A., et al., (1991) Sequences

of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human

Services, NIH Publication No. 91-3242) and DNA fragments encompassing these regions

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can be obtained by standard PCR amplification. The heavy chain constant region can be, for example, an IgG1, IgG2, IgG3, IgG4, IgA, IgE, IgM or IgD constant region, but most preferably is an IgG1 or IgG4 constant region. For a Fab fragment heavy chain gene, the VH-encoding DNA can be operably linked to another DNA molecule encoding only the

5   heavy chain CH1 constant region.

The isolated DNA encoding the VL region can be converted to a full-length light chain gene (as well as a Fab light chain gene) by operably linking the VL-encoding DNA to another DNA molecule encoding the light chain constant region, CL. The sequences of human light chain constant region genes are known in the art (see e.g., Kabat, E. A., et al.,

10   (1991) Sequences of Proteins of immunological Interest, Fifth Edition, U.S. Department of Health and Human Services. NIH Publication No. 91-3242) and DNA fragments encompassing these regions can be obtained by standard PCR amplification. The light chain constant region can be a kappa or lambda constant region, but most preferably is a kappa constant region.

15   To create a scFv gene, the VH- and VL-encoding DNA fragments may be operably linked to another fragment encoding a flexible linker, e.g., encoding the amino acid sequence $(Gly_4-Ser)_3$, such that the VH and VL sequences can be expressed as a contiguous single-chain protein, with the VL and VH regions joined by the flexible linker (see e.g., Bird et al., (1988) Science 242:423-426; Huston et al., (1988) Proc. Natl. Acad. Sci. USA

20   85:5879-5883; McCafferty et al., (1990) Nature 348:552-554), all of which are herein incorporated by reference).

To express the antibodies, or antibody fragments of the invention, DNAs encoding partial or full-length light and heavy chains, obtained as described above, may be inserted into expression vectors such that the genes are operably linked to transcriptional and

25   translational control sequences. In this context, the term "operably linked" is intended to mean that an antibody gene is ligated into a vector such that transcriptional and translational control sequences within the vector serve their intended function of regulating the transcription and translation of the antibody gene. The expression vector and expression control sequences are generally chosen to be compatible with the expression host cell used.

30   The antibody light chain gene and the antibody heavy chain gene can be inserted into separate vectors or, more typically, both genes are inserted into the same expression vector. The antibody genes may be inserted into the expression vector by standard methods (e.g., ligation of complementary restriction sites on the antibody gene fragment and vector, or blunt end ligation if no restriction sites are present). Prior to insertion of the light or heavy

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chain sequences, the expression vector may already carry antibody constant region sequences. For example, one approach to converting the VH and VL sequences to full-length antibody genes is to insert them into expression vectors already encoding heavy chain constant and light chain constant regions, respectively, such that the VH segment is

5   operably linked to the CH segment(s) within the vector and the VL segment is operably linked to the CL segment within the vector. Additionally or alternatively, the recombinant expression vector can encode a signal peptide that facilitates secretion of the antibody chain from a host cell. The antibody chain gene can be cloned into the vector such that the signal peptide is linked in-frame to the amino terminus of the antibody chain gene. The signal

10   peptide can be an immunoglobulin signal peptide or a heterologous signal peptide (i.e., a signal peptide from a non-immunoglobulin protein).

In addition to the antibody chain genes, the recombinant expression vectors of the invention may carry regulatory sequences that control the expression of the antibody chain genes in a host cell. The term "regulatory sequence" is intended to include promoters,

15   enhancers and other expression control elements (e.g., polyadenylation signals) that control the transcription or translation of the antibody chain genes. Such regulatory sequences are described, for example, in Goeddel; Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, Calif. (1990), herein incorporated by reference. It will be appreciated by those skilled in the art that the design of the expression vector, including the

20   selection of regulatory sequences may depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. Preferred regulatory sequences for mammalian host cell expression include viral elements that direct high levels of protein expression in mammalian cells, such as promoters and/or enhancers derived from cytomegalovirus (CMV) (such as the CMV promoter/enhancer), Simian Virus 40 (SV40)

25   (such as the SV40 promoter/enhancer), adenovirus, (e.g., the adenovirus major late promoter (AdMLP)) and polyoma virus. For further description of viral regulatory elements, and sequences thereof, see e.g., U.S. Pat. No. 5,168,062 by Stinski, U.S. Pat. No. 4,510,245 by Bell et al. and U.S. Pat. No. 4,968,615 by Schaffner et al., all of which are herein incorporated by reference.

30   In addition to the antibody chain genes and regulatory sequences, the recombinant expression vectors of the invention may carry additional sequences, such as sequences that regulate replication of the vector in host cells (e.g., origins of replication) and selectable marker genes. The selectable marker gene facilitates selection of host cells into which the vector has been introduced (see e.g., U.S. Pat. Nos. 4,399,216, 4,634,665 and 5,179,017, all

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by Axel et al.). For example, typically the selectable marker gene confers resistance to drugs, such as G418, hygromycin or methotrexate, on a host cell into which the vector has been introduced. Preferred selectable marker genes include the dihydrofolate reductase (DHFR) gene (for use in dhfr- host cells with methotrexate selection/amplification) and the

5   neomycin gene (for G418 selection).

For expression of the light and heavy chains, the expression vector(s) encoding the heavy and light chains may be transfected into a host cell by standard techniques. The various forms of the term "transfection" are intended to encompass a wide variety of techniques commonly used for the introduction of exogenous DNA into a prokaryotic or

10   eukaryotic host cell, e.g., electroporation, calcium-phosphate precipitation, DEAE-dextran transfection and the like.

Preferred mammalian host cells for expressing the recombinant antibodies of the invention include PER.C6™ cells (Crucell, The Netherlands), Chinese Hamster Ovary (CHO cells) (including dhfr- CHO cells, described in Urlaub and Chasin, (1980) Proc. Natl.

15   Acad. Sci. USA 77:4216-4220, used with a DHFR selectable marker, e.g., as described in R. J. Kaufman and P. A. Sharp (1982) Mol. Biol. 159:601-621), NSO myeloma cells, COS cells and SP2 cells. When recombinant expression vectors encoding antibody genes are introduced into mammalian host cells, the antibodies are generally produced by culturing the host cells for a period of time sufficient to allow for expression of the antibody in the

20   host cells or, more preferably, secretion of the antibody into the culture medium in which the host cells are grown. Antibodies can be recovered from the culture medium using standard protein purification methods.

Host cells can also be used to produce portions of intact antibodies, such as Fab fragments or scFv molecules. It will be understood that variations on the above procedure

25   are within the scope of the present invention. For example, it may be desirable to transfect a host cell with DNA encoding either the light chain or the heavy chain of an antibody of this invention. Recombinant DNA technology may also be used to remove some or all of the DNA encoding either or both of the light and heavy chains that is not necessary for binding to hTNF-α. The molecules expressed from such truncated DNA molecules are also

30   encompassed by the antibodies of the invention. In addition, bifunctional antibodies may be produced in which one heavy and one light chain are an antibody of the invention and the other heavy and light chain are specific for an antigen other than hTNF-α by crosslinking an antibody of the invention to a second antibody by standard chemical crosslinking methods.

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In one preferred system for recombinant expression of an antibody, or fragment thereof, a recombinant expression vector encoding both the antibody heavy chain and the antibody light chain is introduced into dhfr- CHO cells by calcium phosphate-mediated transfection. Within the recombinant expression vector, the antibody heavy and light chain

5   genes are each operably linked to enhancer/promoter regulatory elements (e.g., derived from SV40, CMV, adenovirus and the like, such as a CMV enhancer/AdMLP promoter regulatory element or an SV40 enhancer/AdMLP promoter regulatory element) to drive high levels of transcription of the genes. The recombinant expression vector may also carry a DHFR gene, which allows for selection of CHO cells that have been transfected with the

10   vector using methotrexate selection/amplification. The selected transformant host cells are cultured to allow for expression of the antibody heavy and light chains and intact antibody is recovered from the culture medium. Standard molecular biology techniques are used to prepare the recombinant expression vector, transfect the host cells, select for transformants, culture the host cells and recover the antibody from the culture medium.

15   In certain embodiments, the antibodies and antibody fragments of the present invention are produced in transgenic animals. For example, transgenic sheep and cows may be engineered to produce the antibodies or antibody fragments in their milk (see, e.g., Pollock DP, et al., (1999) Transgenic milk as a method for the production of recombinant antibodies. J. Immunol. Methods 231:147-157, herein incorporated by reference). The

20   antibodies and antibody fragments of the present invention may also be produced in plants (see, e.g., Larrick et al., (2001) Production of secretory IgA antibodies in plants. Biomol. Eng. 18:87-94, herein incorporated by reference). Additional methodologies and purification protocols are provided in Humphreys et al., (2001) Therapeutic antibody production technologies: molecules applications, expression and purification, Curr. Opin.

25   Drug Discov. Devel. 4:172-185, herein incorporated by reference. In certain embodiments, the antibodies or antibody fragments of the present invention are produced by transgenic chickens (see, e.g., US Pat. Pub. Nos. 20020108132 and 20020028488, both of which are herein incorporated by reference).

30   **III.   Therapeutic Formulations and Uses**

The TNF-α binding molecules of the present invention (e.g. antibodies and antibody fragments) are useful for treating a subject having a pathology or condition associated with abnormal levels of a substance reactive with a TNF-α binding molecule, such as TNF-α in excess of, or less than, levels present in a normal healthy subject, where such excess or

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diminished levels occur in a systemic, localized or particular tissue type or location in the body. Such tissue types can include, but are not limited to, blood, lymph, CNS, liver, kidney, spleen, heart muscle or blood vessels, brain or spinal cord, white matter or gray matter, cartilage, ligaments, tendons, lung, pancreas, ovary, testes, and prostate. Increased

5   or decreased TNF-α concentrations relative to normal levels can also be localized to specific regions or cells in the body, such as joints, synovium, nerve blood vessel junctions, bones, specific tendons or ligaments, or sites of infection, such as bacterial or viral infections.

TNF-related pathologies include, but are not limited to, the following:

(A) acute and chronic immune and autoimmune pathologies, such as systemic lupus

10   erythematosus (SLE), rheumatoid arthritis, thyroidosis, graft-versus-host disease, scleroderma, diabetes mellitus, Graves' disease, and the like;

(B) sepsis, cachexia, circulatory collapse and/or shock resulting from acute or chronic bacterial, viral parasitic or fungal infections;

(C) inflammatory diseases, such as chronic inflammatory pathologies and vascular

15   inflammatory pathologies, including chronic inflammatory pathologies such as, but not limited to, sarcoidosis, inflammatory bowel disease (i.e., ulcerative colitis and Crohn's disease) and vascular inflammatory pathologies, such as, but not limited to, disseminated intravascular coagulation, atherosclerosis, and Kawasaki's pathology;

(D) neurodegenerative diseases, including, but not limited to, demyelinating

20   diseases, such as multiple sclerosis and acute transverse myelitis; extrapyramidal and cerebellar disorders such as lesions of the corticospinal system; disorders of the basal ganglia; hyperkinetic movement disorders such as Huntington's disease and senile chorea; drug-induced movement disorders, such as those induced by drugs which block CNS dopamine receptors; hypokinetic movement disorders, such as Parkinson's disease;

25   progressive supranuclear palsy; cerebellar and spinocerebellar disorders, such as structural lesions of the cerebellum; spinocerebellar degenerations (spinal ataxia, Friedreich's ataxia, cerebellar cortical degenerations, multiple systems degenerations (Shy-Drager syndrome, , Dejerine-Sottas, and Machado-Joseph diseases)); and systemic disorders (Refsum's disease, , ataxia, telangiectasia, and mitochondrial multi.system disorder); demyelinating core

30   disorders, such as multiple sclerosis, acute transverse myelitis; disorders of the motor unit, such as neurogenic muscular atrophies (anterior horn cell degeneration, such as amyotrophic lateral sclerosis, infantile spinal muscular atrophy and juvenile spinal muscular atrophy); Alzheimer's disease; Down's Syndrome in middle age; Diffuse Lewy body disease; senile dementia of Lewy body type; Wernicke-Korsakoff syndrome; chronic

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alcoholism; Creutzfeldt-Jakob disease; subacute sclerosing panencephalitis, Hallerrorden-Spatz disease; and dementia pugilistica, or any subset thereof;

(E) malignant pathologies involving TNF-secreting tumors or other malignancies involving TNF, such as, but not limited to leukemias (acute, chronic myelocytic, chronic lymphocytic and/or myelodyspastic syndrome); lymphomas (Hodgkin's and non-Hodgkin's lymphomas, such as malignant lymphomas (Burkitt's lymphoma or mycosis fungoides)); and

(F) alcohol-induced hepatitis.

Additional TNF-α pathologies include, but are limited to, psoriasis, psoriatic arthritis, Wegener's granulomatosis, ankylosing spondylitis, heart failure, reperfusion injury, chronic obstructive pulmonary disease, pulmonary fibrosis, and hepatitis C infection. See, e.g., Berkow et al., eds., The Merck Manual, 16th edition, chapter 11, pp 1380-1529, Merck and Co., Rahway, N.J., 1992, herein incorporated by reference.

The TNF-α binding molecules of the present invention may be administered by any suitable means, including parenteral, non-parenteral, subcutaneous, topical, intraperitoneal, intrapulmonary, intranasal, and intralesional administration (e.g., for local immunosuppressive treatment). Parenteral infusions include, but are not limited to, intramuscular, intravenous, intra-arterial, intraperitoneal, or subcutaneous administration. In addition, TNF-α binding molecules are suitably administered by pulse infusion, particularly with declining doses. Preferably, the dosing is given by injections, most preferably intravenous or subcutaneous injections, depending in part on whether the administration is brief or chronic.

Dosage regimens may be adjusted to provide the optimum desired response (e.g., a therapeutic or prophylactic response). For example, a single bolus may be administered, several divided doses may be administered over time or the dose may be proportionally reduced or increased as indicated by the exigencies of the therapeutic situation. It is advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. The dosages of the TNF-α binding molecules of the present invention are generally dependent on (a) the unique characteristics of the active compound and the particular therapeutic or prophylactic effect to be achieved, and (b) the limitations inherent in the art of compounding such an active compound for the treatment of sensitivity in individuals.

An exemplary, non-limiting range for a therapeutically or prophylactically effective amount of an antibody or antibody fragment (or other TNF-α binding molecule of the

invention) is 0.1-20 mg/kg, more preferably 1-10 mg/kg. It is to be noted that dosage values may vary with the type and severity of the condition to be alleviated. It is to be further understood that for any particular subject, specific dosage regimens should be adjusted over time according to the individual need and the professional judgment of the person

5   administering or supervising the administration of the compositions, and that dosage ranges set forth herein are exemplary only and are not intended to limit the present invention.

The dosage administered will, of course, vary depending upon known factors such as the pharmacodynamic characteristics of the particular agent, its mode and route of administration, the age, health, and weight of the recipient, the nature and extent of

10   symptoms, the kind of concurrent treatment, the frequency of treatment, and the effect desired. For example, a daily dosage of active ingredient can be about 0.01 to 100 milligrams per kilogram of body weight. Ordinarily 1.0 to 5, and preferably 1 to 10 milligrams per kilogram per day given in divided doses 1 to 6 times a day or in sustained release form, is effective to obtain desired results.

15   As a non-limiting example, treatment of TNF-related pathologies in humans or animals can be provided as a daily dosage of a TNF-α binding molecule of the present invention of 0.1 to 100 mg/kg, such as 0.5, 0.9, 1.0, 1.1, 1.5, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 40, 45, 50, 60, 70, 80, 90 or 100 mg/kg, per day, on at least one of day 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15,

20   16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40, or alternatively, at least one of week 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20, or any combination thereof, using single or divided doses of every 24, 12, 8, 6, 4, or 2 hours, or any combination thereof.

Dosage forms (compositions) suitable for internal administration generally contain

25   from about 0.1 milligram to about 500 milligrams of active ingredient per unit. In these pharmaceutical compositions the active ingredient will ordinarily be present in an amount of about 0.5-95% by weight based on the total weight of the composition.

The TNF-α binding molecules of the invention can be incorporated into pharmaceutical compositions suitable for administration to a subject. For example, the

30   pharmaceutical composition may comprise a TNF-α binding molecule (e.g. an antibody or antibody fragment) and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" includes solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like that are physiologically compatible. Examples of pharmaceutically acceptable carriers include

one or more of the following: water, saline, phosphate buffered saline, dextrose, glycerol, ethanol and the like, as well as combinations thereof. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, or sodium chloride in the composition. Pharmaceutically acceptable carriers may further

5   comprise minor amounts of auxiliary substances such as wetting or emulsifying agents, preservatives or buffers, which enhance the shelf life or effectiveness of the TNF-α binding molecules.

The compositions of this invention may be in a variety of forms. These include, for example, liquid, semi-solid and solid dosage forms, such as liquid solutions (e.g., injectable

10   and infusible solutions), dispersions or suspensions, tablets, pills, powders, liposomes and suppositories. The preferred form depends on the intended mode of administration and therapeutic application. Typical preferred compositions are in the form of injectable or infusible solutions, such as compositions similar to those used for passive immunization of humans with other antibodies.

15   Therapeutic compositions typically are sterile and stable under the conditions of manufacture and storage. The composition can be formulated as a solution, microemulsion, dispersion, liposome, or other ordered structure suitable to high drug concentration. Sterile injectable solutions can be prepared by incorporating the active compound (i.e., antibody or antibody fragment) in the required amount in an appropriate solvent with one or a

20   combination of ingredients enumerated above, as required, followed by sterile filtration. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-

25   drying that yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof. The proper fluidity of a solution can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prolonged absorption of injectable compositions can be brought about by including in the composition

30   an agent that delays absorption, for example, monostearate salts and gelatin.

In certain embodiments, the active compound may be prepared with a carrier that will protect the compound against rapid release, such as a controlled release formulation, including implants, transdermal patches, and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate,

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polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Many methods for the preparation of such formulations are patented or generally known to those skilled in the art (see, e.g., Sustained and Controlled Release Drug Delivery Systems, J. R. Robinson. ed., Marcel Dekker, Inc., New York, 1978).

5   In certain embodiments, the TNF-α binding molecules of the invention may be orally administered, for example, with an inert diluent or an assimilable edible carrier. The compound (and other ingredients, if desired) may also be enclosed in a hard or soft shell gelatin capsule, compressed into tablets, or incorporated directly into the subject's diet. For oral therapeutic administration, the compounds may be incorporated with excipients and

10   used in the form of ingestible tablets, buccal tablets, troches, capsules, elixirs, suspensions, syrups, wafers, and the like. To administer a compound of the invention by other than parenteral administration, it may be necessary to coat the compound with, or co-administer the compound with, a material to prevent its inactivation.

         Supplementary active compounds can also be incorporated into the compositions. In

15   certain embodiments, a TNF-α binding molecule (e.g. an antibody or antibody fragment) of the invention is coformulated with and/or coadministered with one or more additional therapeutic agents that are useful for treating disorders in which TNF-α activity is detrimental. For example, a TNF-α binding molecule of the invention may be coformulated and/or coadministered with one or more antibodies that bind other targets (e.g., antibodies

20   that bind other cytokines or that bind cell surface molecules), one or more cytokines, soluble TNF-α receptor (see e.g., PCT Publication No. WO 94/06476) and/or one or more chemical agents that inhibit hTNF-α production or activity (such as cyclohexane-ylidene derivatives as described in PCT Publication No. WO 93119751). Furthermore, TNF-α binding molecules of the invention may be used in combination with one or more of the

25   foregoing therapeutic agents. Such combination therapies may advantageously utilize lower dosages of the administered therapeutic agents, thus avoiding possible toxicities or complications associated with the various monotherapies.

         Non-limiting examples of therapeutic agents for rheumatoid arthritis with which the TNF-α binding molecules of the invention can be combined include, but are not limited to

30   the following: non-steroidal anti-inflammatory drug(s) (NSAIDs); cytokine suppressive anti-inflammatory drug(s) (CSAIDs); CDP-571/BAY-10-3356 (humanized anti-TNF-α antibody; Celltech/Bayer); cA2 (chimeric anti-TNF-α antibody; Centocor); 75 kDa TNFR-IgG (75 kDa TNF receptor-IgG fusion protein; Immunex; see e.g., Arthritis & Rheumatism (1994) Vol. 37. S295; J. Invest Med. (1996) Vol. 44 235A); 55 kDa TNFR-IgG (55 kDa

TNF receptor-IgG fusion protein; Hoffmann-LaRoche); IDEC-CE9.I/SB 210396 (non-depleting primatized anti-CD4 antibody; IDEC/SmithKline; see e.g., Arthritis & Rheumatism (1995) Vol. 38, S185); DAB 486-IL-2 and/or DAB 389-IL-2 (IL-2 fusion proteins; Seragen; see e.g., Arthritis & Rheumatism (1993) Vol. 36, 1223); Anti-Tac

5　(humanized anti-IL-2R.alpha; Protein Design Labs/Roche); IL-4 (anti-inflammatory cytokine; DNAX/Schering); IL-10 (SCH 52000; recombinant IL-10, anti-inflammatory cytokine; DNAX/Schering); IL-10 and/or IL-4 agonists (e.g., agonist antibodies); IL-1 RA (IL-1 receptor antagonist; Synergen/Amgen); TNF-bp/s-TNFR (soluble TNF binding protein; see e.g., Arthritis & Rheumatism (1996) Vol. 39 No. 9 (supplement), S284; Heart

10　and Circulatory Physiology (1995) Vol. 268, pp. 3742); R973401 (phosphodiesterase Type IV inhibitor; see e.g., Arthritis & Rheumatism (1996) Vol. 39. No. 9 (supplement), S282); MK-966 (COX-2 Inhibitor; see e.g., Arthritis & Rheumatism (1996) Vol. 3, No. 9 (supplement), S81); Iloprost (see e.g., Arthritis & Rheumatism (1996) Vol. 39. No. 9 (supplement), S82); methotrexate: thalidomide (see e.g., Arthritis & Rheumatism (1996)

15　Vol. 9, No. 9 (supplement), S282) and thalidomide-related drugs (e.g., Celgen); leflunomide (anti-inflammatory and cytokine inhibitor; see e.g., Arthritis & Rheumatism (1996) Vol. 39 No. 9 (supplement), S131; Inflammation Research (1996) Vol. 4, pp. 103-107); tranexamic acid (inhibitor of plasminogen activation; see e.g., Arthritis & Rheumatism (1996) Vol. 39, No. 9 (supplement), S284); T614 (cytokine inhibitor; see e.g., Arthritis & Rheumatism

20　(1996) Vol. 39 No. 9 (supplement), S282); prostaglandin E1 (see e.g., Arthritis & Rheumatism(1996) Vol. 39, No. 9 (supplement), S282); Tenidap (non-steroidal anti-inflammatory drug; see e.g., Arthritis & Rheumatism (1996) Vol. 39 No. 9 (supplement), S280); Naproxen (non-steroidal anti-inflammatory drug; see e.g., Neuro Report (1996) Vol. 7, pp. 1209-1213); Meloxicam (non-steroidal anti-inflammatory drug); Ibuprofen (non-

25　steroidal anti-inflammatory drug); Piroxicam (non-steroidal anti-inflammatory drug); Diclofenac (non-steroidal anti-inflammatory drug); Indomethacin (non-steroidal anti-inflammatory drug); Sulfasalazine (see e.g., Arthritis & Rheumatism (1996) Vol. 9, No. 9 (supplement), S281); Azathioprine (see e.g., Arthritis & Rheumatism (1996) Vol. 39 No. 9 (supplement), S281); ICE inhibitor (inhibitor of the enzyme interleukin-1 beta converting

30　enzyme); zap-70 and/or Ick inhibitor (inhibitor of the tyrosine kinase zap-70 or Ick); VEGF inhibitor and/or VEGF-R inhibitor (inhibitors of vascular endothelial cell growth factor or vascular endothelial cell growth factor receptor; inhibitors of angiogenesis); corticosteroid anti-inflammatory drugs (e.g., SB203580); TNF-convertase inhibitors; anti-IL-12 antibodies; interleukin-11 (see e.g., Arthritis & Rheumatism (1996) Vol. 39, No. 9

(supplement), S296); interleukin-13 (see e.g., Arthritis & Rheumatism (1996) Vol. 39, No. 9 (supplement), S308); interleukin-17 inhibitors (see e.g., Arthritis & Rheumatism (1996) Vol. 39. No. 9 (supplement), S120); gold; penicillamine; chloroquine; hydroxychloroquine; chlorambucil; cyclophosphamide; cyclosporine; total lymphoid irradiation; anti-thymocyte

5   globulin; anti-CD4 antibodies; CD5-toxins; orally-administered peptides and collagen; lobenzarit disodium; Cytokine Regulating Agents (CRAs) HP228 and HP466 (Houghten Pharmaceuticals, Inc.); ICAM-1 antisense phosphorothioate oligodeoxynucleotides (ISIS 2302; Isis Pharmaceuticals, Inc.); soluble complement receptor 1 (TP10; T Cell Sciences, Inc.); prednisone. orgotein; glycosaninoglycan polysulphate; minocycline; anti-IL-2R

10   antibodies; marine and botanical lipids (fish and plant seed fatty acids; see e.g., DeLuca et al. (1995) Rheum. Dis. Clin. North Am. 21:759-777); auranofin; phenylbutazone; meclofenamic acid; flufenamic acid; intravenous immune globulin; zileuton; mycophenolic acid (RS-61443); tacrolimus (FK-506); sirolimus (rapamycin); amiprilose (therafectin); cladribine (2-chlorodeoxyadenosine); azaribine, and the D2E7 antibody (See, US Pat.

15   6,258,562, herein incorporated by reference).

Non-limiting examples of therapeutic agents for inflammatory bowel disease with which the TNF-α binding molecules of the invention can be combined include, but are not limited to, the following: budenoside; epidermal growth factor; corticosteroids; cyclosporin, sulfasalazine; aminosalicylates; 6-mercaptopurine; azathioprine; metronidazole;

20   lipoxygenase inhibitors; mesalamine; olsalazine; balsalazide; antioxidants; thromboxane inhibitors; IL-1 receptor antagonists; anti-IL-1beta monoclonal antibodies; anti-IL-6 monoclonal antibodies; growth factors; elastase inhibitors; pyridinyl-imidazole compounds; CDP-571/BAY-10-3356 (humanized anti-TNF-α antibody; Celltech/Bayer); cA2 (chimeric anti-TNF-α antibody; Centocor); 75 kDa TNFR-IgG (75 kDa TNF receptor-IgG fusion

25   protein; Immunex; see e.g., Arthritis & Rheumatism (1994) Vol. 7, S295; J. Invest. Med. (1996) Vol. 44 235A); 55 kDa TNFR-IgG (55 kDa TNF receptor-IgG fusion protein; Hoffmann-LaRoche); interleukin-10 (SCH 52000; Schering Plough); IL-4 (anti-inflammatory cytokine; DNAX/Schering); IL-10 and/or IL4 agonists (e.g., agonist antibodies); interleukin-11; glucuronide- or dextran-conjugated prodrugs of prednisolone,

30   dexamethasone or budesonide; ICAM-1 antisense phosphorothioate oligodeoxynucleotides (ISIS 2302; Isis Pharmaceuticals, Inc.); soluble complement receptor 1 (TP10; T Cell Sciences, Inc.); slow-release mesalazine; methotrexate; antagonists of Platelet Activating Factor (PAF); ciprofloxacin; and lignocaine.

Non-limiting examples of therapeutic agents for multiple sclerosis with which the TNF-α binding molecules of the invention can be combined include, but are not limited to, the following: corticosteroids; prednisolone; methylprednisolone; azathioprine; cyclophosphamide; cyclosporine; methotrexate; 4-aminopyridine; tizanidine; interferon-

5   beta1a (Avonex.TM.; Biogen); interferon-beta1b (Betaseron.TM.; Chiron/Berlex); Copolymer 1 (Cop1; Copaxone.TM.; Teva Pharmaceutical Industries, Inc.); hyperbaric oxygen; intravenous immunoglobulin; clabribine; CDP-571/BAY-10-3356 (humanized anti-TNF-α antibody; Celltech/Bayer); cA2 (chimeric anti-TNF-α antibody; Centocor); 75 kDa TNFR-IgG (75 kDa TNF receptor-IgG fusion protein; Immunex; see e.g., Arthritis &

10   Rheumatism (1994) Vol. 37, S295; J Invest. Med. (1996) Vol. 44, 235A); 55 kDa TNFR-IgG (55 kDa TNF receptor-IgG fusion protein; Hoffmann-LaRoche); IL-10; IL-4 (anti-inflammatory cytokine; DNAX/Schering); and IL-10 and/or IL-4 agonists (e.g., agonist antibodies).

Non-limiting examples of therapeutic agents for sepsis with which the TNF-α

15   binding molecules of the invention can be combined include, but are not limited to, the following: hypertonic saline solutions; antibiotics; intravenous gamma globulin; continuous hemofiltration; carbapenems (e.g., meropenem); antagonists of cytokines such as TNF-α, IL-6 and/or IL-8; CDP-571/BAY-10-3356 (humanized anti-TNF-α antibody; Celltech/Bayer); cA2 (chimeric anti-TNF-α antibody; Centocor); 75 kDa TNFR-IgG (75

20   kDa TNF receptor-IgG fusion protein; Immunex; see e.g., Arthritis & Rheumatism (1994) Vol. 37, S295; J Invest. Med. (1996) Vol. 44, 235A); 55 kDa TNFR-IgG (55 kDa TNF receptor-IgG fusion protein; Hoffmann-LaRoche); Cytokine Regulating Agents (CRAs) HP228 and HP466 (Houghten Pharmaceuticals, Inc.); SK&F 107647 (low molecular peptide; SmithKline Beecham); tetravalent guanylhydrazone CNI-1493 (Picower Institute);

25   Tissue Factor Pathway Inhibitor (TFPI; Chiron); PHP (chemically modified hemoglobin; APEX Bioscience); iron chelators and chelates, including diethylenetriamine pentaacetic acid-iron (III) complex (DTPA iron (III); Molichem Medicines); lisofylline (synthetic small molecule methylxanthine; Cell Therapeutics, Inc.); PGG-Glucan (aqueous soluble β-1,3 glucan; Alpha-Beta Technology); apolipoprotein A-1 reconstituted with lipids; chiral

30   hydroxamic acids (synthetic antibacterials that inhibit lipid A biosynthesis); anti-endotoxin antibodies; E5531 (synthetic lipid A antagonist; Eisai America, Inc.); rBPI21 (recombinant N-terminal fragment of human Bactericidal/Permeability-Increasing Protein); the D2E7 antibody, and Synthetic Anti-Endotoxin Peptides (SAEP; Bios Ynth Research Laboratories).

Non-limiting examples of therapeutic agents for adult respiratory distress syndrome (ARDS) with which the TNF-α binding molecules of the invention can be combined include the following: anti-IL-8 antibodies; surfactant replacement therapy; CDP-571/BAY-10-3356 (humanized anti-TNF-α antibody; Celltech/Bayer); cA2 (chimeric anti-TNF-α antibody; Centocor); 75 kDa TNFR-IgG (75 kDa TNF receptor-IgG fusion protein; Immunex; see e.g., Arthritis & Rheumatism (1994) Vol. 3.7 S295; J. Invest. Med. (1996) Vol. 44, 235A); and 55 kDa TNFR-IgG (55 kDa TNF receptor-IgG fusion protein; Hoffmann-LaRoche).

The pharmaceutical compositions of the invention may include a "therapeutically effective amount" or a "prophylactically effective amount" of an antibody or antibody fragment of the invention. A "therapeutically effective amount" refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired therapeutic result. A therapeutically effective amount of the antibody or antibody fragment may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of the antibody or antibody fragment to elicit a desired response in the individual. A therapeutically effective amount is also one in which any toxic or detrimental effects of the antibody or antibody fragment are outweighed by the therapeutically beneficial effects. A "prophylactically effective amount" refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired prophylactic result. Typically, since a prophylactic dose is used in subjects prior to or at an earlier stage of disease, the prophylactically effective amount will be less than the therapeutically effective amount.

IV.   Additional TNF-α Binding Molecule Uses

The present invention also provides TNF-α binding molecules (e.g., anti-TNF-α peptides and antibodies) detectably labeled, as described below, for use in diagnostic methods for detecting TNF-α in patients known to be or suspected of having a TNF-α-mediated disease.

TNF-α binding molecules of the present invention, such as anti-TNF-α peptides and/or antibodies are useful for immunoassays which detect or quantify TNF-α in a sample. An immunoassay for TNF-α typically comprises incubating a biological sample in the presence of a detectably labeled high affinity anti-TNF-α peptide and/or antibody of the present invention capable of selectively binding to TNF-α, and detecting the labeled peptide or antibody which is bound in a sample. Various clinical assay procedures are well known

in the art, e.g., as described in Immunoassays for the 80's, A. Voller et al., eds., University
Park, 1981.

Thus, an anti-TNF peptide or antibody, can be captured on nitrocellulose, or on any
other solid support which is capable of immobilizing soluble proteins. A TNF-α-containing

5   sample is then added to the support which is subsequently washed with suitable buffers to
remove unbound proteins. A second, detectably labeled, TNF-α specific peptide or
antibody is added to the solid phase support that can then be washed with the buffer a
second time to remove unbound detectably labeled peptide or antibody. The amount of
bound label on the solid support can then be detected by known methods.

10   By "solid phase support" or "carrier" is intended any support capable of binding
peptide, antigen or antibody. Well-known supports or carriers, include glass, polystyrene,
polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses,
polyacrylamides, agaroses, and magnetite. The nature of the carrier can be either soluble to
some extent or insoluble for the purposes of the present invention. The support material can

15   have virtually any possible structural configuration so long as the coupled molecule retains
its ability to bind to TNF-α. Thus, the support configuration can be spherical, as in a bead,
or cylindrical, as in the inside surface of a test tube, or the external surface of a rod.
Alternatively, the surface can be flat such as a sheet, culture dish, test strip, microtiter
plates, etc. Preferred supports include polystyrene beads. Those skilled in the art will know

20   many other suitable carriers for binding antibody, peptide or antigen, or can ascertain the
same by routine experimentation. Well known methods can be used to determine the
binding activity of a given lot of anti-TNF-α peptide and/or antibody. Those skilled in the
art can determine operative and optimal assay conditions by routine experimentation.

Detectably labeling a TNF-α binding molecule, such as a TNF-specific peptide

25   and/or antibody, can be accomplished by coupling to an enzyme for use in an enzyme
immunoassay (EIA), or enzyme-linked immunosorbent assay (ELISA). The linked enzyme
reacts with the exposed substrate to generate a chemical moiety which can be detected, for
example, by spectrophotometric, fluorometric or by visual means. Enzymes which can be
used to detectably label the TNF-α binding molecules of the present invention include, but

30   are not limited to, malate dehydrogenase, staphylococcal nuclease, delta-5-steroid
isomerase, yeast alcohol dehydrogenase, alpha-glycerophosphate dehydrogenase, triose
phosphate isomerase, horseradish peroxidase, alkaline phosphatase, asparaginase, glucose
oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate
dehydrogenase,

52

glucoamylase and acetylcholinesterase.

By radioactively labeling the TNF-α binding molecules, it is possible to detect TNF-α through the use of a radioimmunoassay (RIA) (see, for example, Work, et al., (1978) Laboratory Techniques and Biochemistry in Molecular Biology, North Holland Publishing Company, N.Y.). The radioactive isotope can be detected by such means as the use of a gamma counter or a scintillation counter or by autoradiography.

It is also possible to label the TNF-α binding molecules with a fluorescent compound. When the fluorescently labeled molecule is exposed to light of the proper wave length, its presence can then be detected due to fluorescence. Among the most commonly used fluorescent labeling compounds are fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, o-phthaldehyde and fluorescamine.

The TNF-α binding molecules can also be detectably labeled using fluorescence-emitting metals such as ^{125}Eu, or others of the lanthanide series. These metals can be attached to the TNF-α binding molecule using such metal chelating groups as diethylenetriaminepentaacetic acid (DTPA) or ethylenediamine-tetraacetic acid (EDTA).

The TNF-α binding molecules also can be detectably labeled by coupling to a chemiluminescent compound. The presence of the chemiluminescently labeled molecule is then determined by detecting the presence of luminescence that arises during the course of a chemical reaction. Examples of particularly useful chemiluminescent labeling compounds are luminol, isoluminol, theromatic acridinium ester, imidazole, acridinium salt and oxalate ester.

Likewise, a bioluminescent compound can be used to label the TNF-α binding molecules of the present invention. Bioluminescence is a type of chemiluminescence found in biological systems in which a catalytic protein increases the efficiency of the chemiluminescent reaction. The presence of a bioluminescent protein is determined by detecting the presence of luminescence. Important bioluminescent compounds for purposes of labeling are luciferin, luciferase and aequorin.

Detection of the TNF-α binding molecules can be accomplished by a scintillation counter, for example, if the detectable label is a radioactive gamma emitter, or by a fluorometer, for example, if the label is a fluorescent material. In the case of an enzyme label, the detection can be accomplished by colorometric methods which employ a substrate for the enzyme. Detection can also be accomplished by visual comparison of the extent of enzymatic reaction of a substrate to similarly prepared standards.

In some embodiments of the present invention, the TNF-α which is detected by the above assays can be present in a biological sample. Any sample containing TNF-α can be used. Preferably, the sample is a biological fluid such as, for example, blood, serum, lymph, urine, cerebrospinal fluid, amniotic fluid, synovial fluid, a tissue extract or

5   homogenate, and the like. However, the invention is not limited to assays using only these samples, as it is possible for one of ordinary skill in the art to determine suitable conditions which allow the use of other samples.

In situ detection can be accomplished by removing a histological specimen from a patient, and providing the combination of labeled TNF-α binding molecules of the present

10 invention to such a specimen. The TNF-α binding molecule is preferably provided by applying or by overlaying the labeled TNF-α binding molecule to a biological sample. Through the use of such a procedure, it is possible to determine not only the presence of TNF-α but also the distribution of TNF-α in the examined tissue. Using the present invention, those of ordinary skill will readily perceive that any of a wide variety of

15 histological methods (such as staining procedures) can be modified in order to achieve such in situ detection.

The TNF-α binding molecules of the present invention can be adapted for utilization in an immunometric assay, also known as a "two-site" or "sandwich" assay. In a typical immunometric assay, a quantity of unlabeled TNF-α binding molecule (such as an anti-

20 TNF-α antibody) is bound to a solid support that is insoluble in the fluid being tested and a quantity of detectably labeled soluble antibody is added to permit detection and/or quantitation of the ternary complex formed between solid-phase antibody, antigen, and labeled antibody.

Typical, and preferred, immunometric assays include "forward" assays in which the

25 TNF-α binding molecule (e.g. antibody) bound to the solid phase is first contacted with the sample being tested to extract the TNF-α from the sample by formation of a binary solid phase antibody-TNF-α complex. After a suitable incubation period, the solid support is washed to remove the residue of the fluid sample, including unreacted TNF-α, if any, and then contacted with the solution containing a known quantity of labeled antibody (which

30 functions as a "reporter molecule"). After a second incubation period to permit the labeled antibody to complex with the TNF-α bound to the solid support through the unlabeled antibody, the solid support is washed a second time to remove the unreacted labeled antibody. This type of forward sandwich assay can be a simple "yes/no" assay to determine whether TNF-α is present or can be made quantitative by comparing the measure of labeled

antibody with that obtained for a standard sample containing known quantities of TNF-α. Such "two-site" or "sandwich" assays are described by Wide (Radioimmune Assay Method, Kirkham, ed., Livingstone, Edinburgh, 1970, pp. 199-206).

5   Other types of "sandwich" assays, which can also be useful with TNF-α, are the so-called "simultaneous" and "reverse" assays. A simultaneous assay involves a single incubation step wherein the antibody bound to the solid support and labeled antibody are both added to the sample being tested at the same time. After the incubation is completed, the solid support is washed to remove the residue of fluid sample and uncomplexed labeled antibody. The presence of labeled antibody associated with the solid support is then

10   determined as it would be in a conventional "forward" sandwich assay. In the "reverse" assay, stepwise addition first of a solution of labeled antibody to the fluid sample followed by the addition of unlabeled antibody bound to a solid support after a suitable incubation period, is utilized. After a second incubation, the solid phase is washed in conventional fashion to free it of the residue of the sample being tested and the solution of unreacted

15   labeled antibody. The determination of labeled antibody associated with a solid support is then determined as in the "simultaneous" and "forward" assays.

       In some embodiments, the TNF-α binding molecules of this invention, attached to a solid support, can be used to remove TNF-α from fluids or tissue or cell extracts. In a preferred embodiment, they are used to remove TNF-α from blood or blood plasma

20   products. In another preferred embodiment, the TNF-α binding molecules are advantageously used in extracorporeal immunoadsorbent devices, which are known in the art (see, for example, Seminars in Hematology, 26 (2 Suppl. 1)(1989)). Patient blood or other body fluid is exposed to the attached TNF-α binding molecule, resulting in partial or complete removal of circulating TNF-α (free or in immune complexes), following which the

25   fluid is returned to the body. This immunoadsorption can be implemented in a continuous flow arrangement, with or without interposing a cell centrifugation step. See, for example, Terman, et al., (1976) J. Immunol. 117:1971-1975.

EXPERIMENTAL

30   The following examples are provided in order to demonstrate and further illustrate certain preferred embodiments and aspects of the present invention and are not to be construed as limiting the scope thereof.

       In the experimental disclosure which follows, the following abbreviations

apply: M (molar); mM (millimolar); nM (nanomolar); pM (picomolar); mg (milligrams); μg (micrograms); pg (picograms); ml (milliliters); μl (microliters); °C (degrees Celsius); OD (optical density); nm (nanometer); BSA (bovine serum albumin); and PBS (phosphate-buffered saline solution).

5

EXAMPLE 1

Construction and Screening of Anti-TNF-α Fab Fragments with Synthetic CDRs and Human Frameworks

This example describes the construction of anti-TNF-α Fab fragments with fully

10   human framework regions and synthetic CDRs. The nucleic acid sequences encoding the hu1 CDRs and framework regions are shown in SEQ ID NOs: 2 and 4, respectively. The six hu1 CDRs employed were as follows: CDRL1 (SEQ ID NO:10); CDRL2 (SEQ ID NO: 20); CDRL3 (SEQ ID NO: 34); CDRH1 (SEQ ID NO: 36); CDRH2 (SEQ ID NO: 44); and CDRH3 (SEQ ID NO: 54).

15   In order to identify mutations that improve the binding properties of hu1, libraries of synthetic CDRs were inserted into a deletion template as described below. Standard mutagenesis techniques (Kunkel, T.A., (1985) Proc. Natl. Acad. Sci. USA, 82: 488-492, herein incorporated by reference) were employed to individually replace each hu1 CDR with a pool of mutagenic oligonucleotides. In this example, the CDRs include residues that

20   encompass both the Kabat and Chothia definitions (e.g., residues 26-35 for CDRH1). The length of CDRH2 made it necessary to construct two separate libraries to cover the entire region.

Mutagenic oligonucleotides were annealed to a uridinylated phage template in which the corresponding hu1 CDR was deleted. This template was composed of the hu1 light chain variable region sequence (SEQ ID NO: 2, with the appropriate hu1 CDR deleted) and

25   the human CL sequence shown in SEQ ID NO: 85 as well as the hu1 heavy chain variable region sequence (SEQ ID NO: 4, with the appropriate hu1 CDR deleted) and the human CH1 sequence shown in SEQ ID NO: 86.

Annealing was accomplished by incubating the reaction at 75 °C for 5 minutes

30   followed by slow cooling to 20 °C over the course of 45 minutes. The annealed samples were placed on ice and T4 DNA polymerase and T4 DNA ligase were added to generate double stranded DNA and the reaction was incubated for 5 minutes at 4 °C followed by 90 minutes at 37 °C. The reaction was phenol extracted, ethanol precipitated and the DNA was electroporated into DH10B cells. XL1 Blue cells were added to the reaction to allow phage

56

amplification before the libraries were plated. Phage stocks were prepared by the addition of 8 ml of growth medium to the plates followed by incubation at 4 °C for a minimum of 4 hours. The phage-containing medium was harvested and clarified by centrifugation and sodium azide (0.02%) was added as a preservative.

5   Initial screening of the anti-TNF-α Fab libraries was done by a plaque lift as described in Watkins, J.D. et al., (1998) Anal. Biochem., 256: 169-177, herein incorporated by reference. Briefly, nitrocellulose filters were coated with goat anti-human kappa antibodies, blocked with 1% BSA and placed on plates containing plaques generated from the phage libraries for 16 hours at 22 °C. Filters were then rinsed in PBS and incubated

10   with varying concentrations of biotinylated human TNF-α for varying lengths of time. Filters were washed in PBS containing 0.1% Tween 20, incubated with NeutrAvidin alkaline phosphatase conjugate for 2-60 minutes and washed in the same buffer. Differences in signal intensity revealed by the addition of standard colorimetric subtrates for alkaline phosphatase were used to identify variants with improved binding properties. This screening

15   procedure resulted in the identification of several Fab fragments that were further characterized as follows:

Positive plaques were picked with a Pasteur pipet and phages were eluted for 1 hour at 37 °C in 100 μl of 10 mM Tris HCl, pH 7.4 and 100 mM NaCl. High titer stocks were then obtained by standard amplification techniques. XL1 Blue cells were grown to an OD_{600} of 1

20   and IPTG was added to a final concentration of 1 mM. Following infection of 15 ml of bacterial culture with 10 μl of high titer phage stock, cells were incubated at 37 °C for an hour and at 22 °C for 16 hours. Bacteria were harvested and washed with 30 mM Tris HCl, pH 8 and 150 mM NaCl. The pellet was resuspended in 640 μl of 30 mM Tris HCl, pH 8, 2 mM EDTA and 20% sucrose and incubated at 4 °C for 15 minutes. Lysed cells were

25   pelleted and the supernatant containing the periplasmic content and Fab fragments was assayed in an ELISA format to determine approximate off-rates. COSTAR #3366 microtiter plates were coated with 1 μg/ml of hTNF-α in carbonate buffer for 16 hours at 4 °C. The plates were washed 3 times with PBS containing 0.1% Tween 20 and blocked with 1% BSA for 1 hour at 22 °C. Fab fragments released from the periplasmic space were

30   serially diluted in PBS containing 0.05% Tween 20 and added to the plates for 1 hour at 22 °C. The plates were washed and incubated with goat anti-human kappa antibodies conjugated to alkaline phosphatase in PBS containing 0.05% Tween 20 for 1 hour at 22 °C. The plates were then washed with PBS containing 0.1% Tween 20 and developed with

standard colorimetric substrates for alkaline phosphatase (see, e.g., Watkins, J.D. et al.,

(1997) Anal. Biochem., 253: 37-45, herein incorporated by reference).

     ELISA assays were also used to determine approximate on-rates. COSTAR #3366

microtiter plates were coated with 2 µg/ml of goat anti-human kappa antibodies in carbonate

5   buffer for 16 hours at 4 °C. Fab fragments released from the periplasmic space were

serially diluted in PBS containing 0.05% Tween 20 and added to wells and incubated for 1

hour at 22 °C. The plates were washed 3 times with PBS containing 0.1% Tween 20 and

incubated with 5 nM biotinylated hTNF-α for 2 minutes at 22 °C. The plates were washed

once and NeutrAvidin alkaline phosphatase conjugate was added for 2 minutes at 22 °C.

10   The plates were washed and developed as above. The initial filter lift screening procedure

and the subsequent characterization of the positive variants in ELISA assays revealed single

amino acid changes in the individual CDRs of several Fab fragments that result in an

increase in affinity for TNF-α in the context of fully human frameworks. These amino acid

changes are listed in Table 1, Table 2 and Table 3.

15   A library where the single beneficial mutations were combined to assess their

additivity was constructed using the procedure described above. This library was screened

using the three assays described in the previous sections and a panel of combinatorial

variants with improved binding properties is shown in Figure 7. The names of the particular

clones identified are provided in Table 4 below, along with the beneficial mutations

20   (defined by the original residue in hu1 followed by the new residue in the particular clone).

TABLE 4

Clone	Light chain mutations	Heavy chain mutations
2C6K	S31L, S54Y	T28K, E61R
2C6P	S31L, S54Y	T28P, E61R
2E7K	S31L, M55R	T28K, I53M, E61R
2E7P	S31L, M55R	T28P, I53M, E61R
A9K	S31M, M55K	T28K, I53M, E61R
A9P	S31M, M55K	T28P, I53M, E61R
A10K	S31Y, M55R	T28K, I53M
A10P	S31Y, M55R	T28P, I53M

Next, binding kinetics of three of the Fab fragments described in Table 4 were

determined in a kinetic exclusion assay. Affinity measurements were performed on a

KinExA™3000 instrument (Sapidyne Instruments, Inc., Boise, Idaho) using Fab fragments (A10K, A9K, and A10P) released from the periplasmic space whose concentration was determined by a quantitative ELISA. Briefly, antigen and antibody fragment were allowed to react in solution and the fraction of unbound reagent was determined by capture and
5　measured on a bead support. Binding kinetics can be determined or calculated from the amount of unbound reagent. For instance, after interaction between TNF-α and a Fab fragment has occurred in solution, binding of the unreacted, free Fab fragment to TNF-α coated beads can be measured on the instrument by detection with a labeled secondary antibody to the Fab fragment (e.g., a goat anti-IgG (heavy and light)). To measure K_d,
10　individual tubes containing a constant concentration of Fab fragment with decreasing concentrations of human TNF-α were incubated for 20 hours at 20 °C in PBS supplemented with 0.1% BSA. A total of 13 tubes were used for each K_d determination. For A10K and A10P, the Fab concentration was 10 pM with the human TNF-α concentration beginning at 160 pM and then serially diluted to 0.078 pM with the final tube containing no human TNF-
15　α. A9K incubation was set in a similar manner, with the Fab at a constant concentration of 20 pM and human TNF-α serially diluted beginning at 500 pM with a final concentration of 0.24 pM. After the incubation, the amount of unbound Fab in the equilibrated samples was determined on the KinExA™3000 instrument according to the manufacturer's instructions. K_d values were determined by the instrument software. The results are provided in Table 5.
20　　　　　To measure k_{on}, individual Fab fragments at a concentration of 40 pM were mixed with 400 pM of hTNF-α. A series of measurements were taken over a time course. The resulting data was used to calculate the k_{on} with the instrument software. k_{off} was calculated by using the formula $K_d = k_{off}/k_{on}$. The results are provided in Table 5.

25　　　　　　　　　　　　　　　　　　　　**TABLE 5**

Clone	K_d (pM)	k_{on} ($M^{-1}sec^{-1}$)	k_{off} (sec^{-1})
A10K	3.5 – 7.2	$3.92 – 7.51 \times 10^6$	$1.96 – 3.76 \times 10^{-5}$
A9K	2.4	2.6×10^6	6.2×10^{-6}
A10P	2.0	4.1×10^6	8.2×10^{-6}

35

EXAMPLE 2

Characterization of Anti-TNF-α Binding Molecules with
Improved Binding Properties

This example describes various in vitro testing procedures used to identify particular

5   characteristics of the eight anti-TNF-α binding molecules from Example 1. First, the ability

of these Fab fragments to prevent TNF-α-mediated cell death was assessed by evaluating

their protective effects on L929 mouse fibroblasts. Specifically, L929 mouse fibroblast

cells were distributed in individual wells in a 96-well plate at a density of 20,000 cells per

well and maintained according to ATCC recommendations. After overnight incubation, Fab

10   fragments released from the periplasmic space were serially diluted in culture medium,

sterile filtered and 50 µl were added to the wells along with actinomycin D to a final

concentration of 1 µg/ml. Immediately thereafter, hTNF-α was added to a final

concentration of 80 pg/ml and the plates were placed in a humidified incubator at 37 °C in a

5% CO_2 atmosphere. After overnight incubation, the protective effects of the various Fab

15   fragments were assessed by monitoring cell survival using the Cell Titer 96®AQueous One

solution reagent (Promega, Madison WI) according to the manufacturer's instructions. The

optical density of individual wells was measured at 490 nm and the results are shown in

Figure 8. At the TNF-α concentration used, approximately 90% of L929 cells died after

overnight incubation and the addition of an unrelated control Fab fragment did not confer

20   any protection. In contrast, each of the eight anti-TNF-α Fab fragments described in Table

4 was able to prevent cell death. Among these TNF-α binding molecules, A10K and A10P

were able to protect cells at the lowest concentration, reflecting improved binding properties

for TNF-α. The effective concentration (EC_{50}) was determined using the curve fitting

function and EC_{50} derivation capabilities of the SigmaPlot® software (SPSS Science,

25   Chicago, IL). In the experiment shown in Figure 8, the EC_{50} of the A10K Fab fragment was

estimated at approximately 25 pM.

In order to further evaluate clones in Table 4 (e.g. A10K) as full IgG molecules,

instead of Fab fragments, the following procedure may be employed. First, the light chain

variable region (VL) and the heavy chain variable region (VH) can be transferred from the

30   A10K Fab expressing phage into, for instance, an expression vector containing both the

heavy and light chain constant regions. Alternatively, the variable regions can be cloned

into two separate expression vectors, each vector eventually expressing only one of the two

chains. The VL region can be amplified by PCR using the following primers: VL 5' primer:

TGGCTCCCAGGTGCCAAATGTGAAATTGTGCTGACTCAG (SEQ ID NO:109); VL

5' biotinylated primer: Biotin-TGGCTCCCAGGTGCCAAATGT (SEQ ID NO:110); and

VL 3' primer: GACAGATGGTGCAGCCACAGT (SEQ ID NO:111). Similarly, the VH

region can be amplified using the following primers (VH 5' primer:

CTCTCCACAGGTGTCCACT CCCAGGTCCAACTGCAGGTC (SEQ ID NO:112); VH

5 5' biotinylated primer: Biotin-CTCTCCACAGGTGTCCACTCC (SEQ ID NO:113); and

VH 3' primer: GAAGACCGATGGGCCCTTGGT (SEQ ID NO:114). After PCR

amplification, the biotinylated DNA strand is removed and the non-biotinylated strand is

annealed to single stranded uridinylated template prepared from the expression vector at an

annealing ratio of 20:1, followed by synthesis with T4 DNA polymerase in presence of T4

10 DNA ligase. In DH10B cells, the uridinylated template is lost, yielding a double stranded

plasmid with, for instance, the A10K IgG.

　　　Next, mammalian cells (e.g., CHO-K1 cells) are transfected with the expression

vector(s) and a pool of stable integrants can be selected by culturing the transfected cells in

an appropriate medium and under appropriate selection. Upon confirmation of IgG

15 expression by ELISA, the pool can be expanded, for instance in roller bottles, and

maintained in selection. The medium is usually changed once every other day and the

conditioned medium containing the A10K IgG is used for IgG purification. This same

procedure may be employed to generate a hu1 IgG or any other IgG molecule.

　　　The L929 cell protection assay was used to characterize A10K and hu1 both as Fab

20 fragments and as intact IgG molecules, along with a control Fab and a control IgG. The

assay was performed as described in the previous section. As shown in Figure 9, both TNF-

α binding molecules, either as Fab fragments or as intact IgGs, were able to protect cells

from the detrimental effects of TNF-α. However, the concentration of A10K necessary to

achieve identical protection is significantly lower than that of hu1, showing that the

25 improvements in binding properties achieved by protein engineering translate into lower

effective doses on cells. In this experiment, the EC_{50} of the A10K Fab fragment was

estimated at approximately 67 pM.

　　　Figure 10 shows a direct comparison between A10K and REMICADE (Oncology

Supply, Dothan, Alabama), a standard of care in rheumatoid arthritis and Crohn's disease.

30 Similarly, both A10K and Remicade are able to fully protect L929 fibroblasts but A10K is

able to achieve identical protection at drastically lower concentrations, demonstrating that

A10K is a more potent molecule and is more effective at neutralizing TNF-α. The EC_{50} of

the A10K IgG molecule was estimated at approximately 2.7 pM.

EXAMPLE 3

In Vivo Examples with A10K

This example describes two in vivo assays with the A10K intact IgG. In particular, this example describes the in vivo TNF-α neutralizing effects of A10K in mice, as well as

5   the protective effects of A10K on TNF-α mediated polyarthritis in mice.

The TNF-α neutralizing ability of A10K in vivo was evaluated as follows. Female C3H/HeN mice (~ 9 weeks of age) were injected intraperitoneally with recombinant human TNF-α (5 μg/mouse) in combination with the sensitizing agent galactosamine (18 mg/mouse). In untreated mice, these conditions result in approximately 90 percent

10   mortality within 48 hours. The neutralizing effect of A10K was evaluated by injecting mice with 0.8 and 4 mg/kg, intravenously, 24 hours prior to hTNF-α challenge. A10K demonstrated a dose-dependent inhibition of mortality, with complete protection being observed at the higher dose investigated. These results are presented in Figure 11.

The effect of A10K on TNF-α mediated polyarthritis was evaluated as follows.

15   C57BL/6NTac-TgN (TNF) mice transgenic for human hTNF-α develop severe chronic arthritis by approximately 20 weeks of age (Keffer, J. et al., (1991) EMBO J., 10:4025-4031, herein incorporated by reference). A dose escalation study was performed on mice exhibiting very early stage joint swelling (9 weeks of age) to determine the effects of A10K on disease progression. Hind joint width was determined and animals were randomized into

20   groups and balanced for initial joint size. Animals were then injected intraperitoneally with 0.1, 0.3 or 1 mg/kg of A10K or control REMICADE (Oncology Supply, Dothan, Alabama. Joint swelling was monitored weekly by measuring the increase in joint width (joint width at t_x – joint width at t_0). A10K exhibited a dose-dependent inhibition in the progression of polyarthritis and was more effective than REMICADE (Oncology Supply, Dothan,

25   Alabama) at similar doses. These results are presented in Figure 12.

EXAMPLE 4

Generating and Screening of AME 3-2

This example describes the construction of the AME-3-2 antibody. PCR primers

30   were used to convert A10K light chain framework into the human germline framework IGKV1-39 (also known as O2 or DP-K9) that appears frequently in the human population. The heavy chain in AME-3-2 is IGVH3-72 (also known as 3-72 or DP-29). This construct was then mutagenized, screened, and tested in a similar fashion as described in Examples 1 and 2 above. This procedure led to the identification of 6 new CDRs for AME 3-2 (shown

in Figure 15): CDRL1 - SEQ ID NO:93; CDRL2 - SEQ ID NO:95; CDRL3 - SEQ ID
NO:97; CDRH1 - SEQ ID NO:87; CDRH2 - SEQ ID NO:89; and CDRH3 - SEQ ID
NO:91. Figure 15 also shows the full light and heavy chains for the AME 3-2 antibody.

The results of testing AME 3-2 on a KinExA™3000 instrument (Sapidyne

5   Instruments, Inc., Boise, Idaho) is shown in Table 7. Also, the EC_{50} value calculated for
AME 3-2 was found to be similar to A10K.

TABLE 7

Clone	K_d (M)	k_{on} (M⁻¹sec⁻¹)	k_{off} (sec⁻¹)
AME 3-2	10×10^{-15}	2.6×10^6	2.6×10^{-8}

EXAMPLE 5

Use of TNF-α Binding Molecules to Treat a TNF-α Mediated Disease

This example describes the use of TNF-α binding molecules for the therapeutic and
prophylactic treatment of a TNF-α mediated disease in a human patient (e.g., with juvenile
and adult rheumatoid arthritis, psoriatic arthritis, Crohn's disease, inflammatory bowel

20   disease, ulcerative colitis, psoriasis, ankylosing spondylitis, Wegener's granulomatosis and
sepsis). For example, a patient with a TNF-α mediated disease may be administered a
single dose of an anti-TNF-α binding molecule, such as 2C6K, 2C6P, 2E7K, 2E7P, A9K,
A9P, A10K, A10P, AME 3-2, or hu1, intravenously at 1-15 milligrams per kilogram of
patient body weight. This patient, however, may also be given multiple doses over time

25   (e.g. 3 mg/kg over multiple days or weeks). Response to therapy may be monitored to
determine the need for increased or reduced dosage and the need for repeat treatment.
Additional guidance on response to therapy and dosage schedules is found in U.S. Patent
5,698,195, herein incorporated by reference. The patient may also be administered an
immunosuppressant, such as methotrexate, in combination with the TNF-α binding

30   molecule.

All publications and patents mentioned in the above specification are herein
incorporated by reference. Various modifications and variations of the described method
and system of the invention will be apparent to those skilled in the art without departing

from the scope and spirit of the invention. Although the invention has been described in
connection with specific preferred embodiments, it should be understood that the invention
as claimed should not be unduly limited to such specific embodiments. Indeed, various
modifications of the described modes for carrying out the invention which are obvious to

5   those skilled in chemistry, medicine, and molecular biology or related fields are intended to
be within the scope of the following claims.

We Claim:

1.   A composition comprising a TNF-α binding molecule, or a nucleic acid
sequence encoding a TNF-α binding molecule, wherein said TNF-α binding molecule
comprises; i) a CDRL3 sequence comprising SEQ ID NO: 33, and ii) a CDRH3
comprising SEQ ID NO: 53.

2.   The composition of Claim 1, wherein said TNF-α binding molecule further
comprises iii) a CDRL1 sequence comprising SEQ ID NO: 15, and iv) a CDRL2
sequence comprising SEQ ID NO: 25.

3.   The composition of Claim 2, wherein said TNF-α binding molecule further
comprises v) a CDRH1 sequence comprising SEQ ID NO: 37, and vi) a CDRH2
sequence comprising SEQ ID NO: 45.

4.   The composition of Claim 2, wherein said TNF-α binding molecule further
comprises v) a CDRH1 sequence comprising SEQ ID NO: 39, and vi) a CDRH2 sequence
comprising SEQ ID NO: 45.

5.   The composition of Claim 1, wherein said TNF-α binding molecule further
comprises iii) a CDRL1 sequence comprising SEQ ID NO: 13, and iv) a CDRL2
sequence comprising SEQ ID NO: 27.

6.   The composition of Claim 5, wherein said TNF-α binding molecule further
comprises v) a CDRH1 sequence comprising SEQ ID NO: 37, and vi) a CDRH2
sequence comprising SEQ ID NO: 55.

7.   The composition of Claim 1, wherein said TNF-α binding molecule further
comprises a light chain variable region, wherein said light chain variable region
comprises a human germline framework region.

8.   The composition of Claim 1, wherein said TNF-α binding molecule further
comprises a heavy chain variable region, wherein said heavy chain variable region
comprises a human germline framework region.

9.   A composition comprising a TNF-α binding, or a nucleic acid sequence encoding a TNF-α binding molecule, wherein said TNF-α binding molecule neutralizes human TNF-α cytotoxicity in an in vitro, cell-based assay with an EC_{50} of 2.0×10^{-11} or less.

5

10.   The composition of Claim 9, wherein said TNF-α binding molecule has a binding affinity (K_d) for human TNF-α of 7.5×10^{-12} M or less.

11.   The composition of Claim 9, wherein said TNF-α binding molecule has an

10   association rate (kon) for human TNF-α of 3.0×10^{6} M^{-1} s^{-1} or greater.

12.   The composition of Claim 9, wherein said TNF-α binding molecule has a dissociation rate (koff) for human TNF-α of 1.0×10^{-4} s^{-1} or less.

15   13.   The composition of Claim 9, wherein said TNF-α binding molecule comprises a light chain variable region, wherein said light chain variable region comprises a human germline framework region.

14.   The composition of Claim 9, wherein said TNF-α binding molecule

20   comprises a heavy chain variable region, wherein said heavy chain variable region comprises a human germline framework region.

15.   A method treating a TNF-α mediated disease comprising;
    a)   providing;

25   i)   a subject, and
        ii)   a composition, wherein said composition comprises TNF-α binding molecules that neutralize human TNF-α cytotoxicity in an in vitro, cell-based assay with an EC_{50} of 2.0×10^{-11} or less; and
    b)   administering said composition to said subject.

30

16.   The method of Claim 15, wherein said TNF-α mediated disease is selected from sepsis, an autoimmune disease, and rheumatoid arthritis.

17.   The method of Claim 15, wherein said TNF-α binding molecules have a binding affinity (K_d) for human TNF-α of 7.5×10^{-12} M or less.

18.   The method of Claim 15, wherein said TNF-α binding molecules have an association rate (kon) for human TNF-α of 3.0×10^6 M^{-1} s^{-1} or greater.

19.   The method of Claim 15, wherein said TNF-α binding molecules have a disassociation rate (koff) for human TNFα of 1.0×10^{-4} s^{-1} or less.

20.   The method of Claim 15, wherein said TNF-α binding molecule comprises a light chain variable region, wherein said light chain variable region comprises a human germline framework region.

21.   The method of Claim 15, wherein said TNF-α binding molecule comprises a heavy chain variable region, wherein said heavy chain variable region comprises a human germline framework region.

22.   A composition comprising a TNF-α binding molecule, or a nucleic acid sequence encoding a TNF-α binding molecule, wherein said TNF-α binding molecule comprises at least one of the following CDR sequences; i) a CDRL1 sequence comprising SEQ ID NO:93; ii) a CDRL2 sequence comprising SEQ ID NO:95; iii) a CDRL3 sequence comprising SEQ ID NO: 97; iv) a CDRH1 sequence comprising SEQ ID NO:87; v) a CDRH2 sequence comprising SEQ ID NO:89, and vi) a CDRH3 sequence comprising SEQ ID NO: 91.

23.   The composition of Claim 22, wherein said TNF-α binding molecule comprises at least three of said CDR sequences.

24.   The composition of Claim 22, wherein said TNF-α binding molecule comprises all six of said CDR sequences.

FIGURE 1

A.

SEQ ID NO:1 - Hu1 light chain variable region amino acid sequence

EIVLTQSPDFQSVTPKEKVTITCRASQFVGSSIHWYQQKPDQSPKLLIKYASESMS
GVPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSHSWHFTFGQGTKVEIK

B.

SEQ ID NO:2 - Hu1 light chain variable region nucleic acid sequence

GAAATTGTGCTGACTCAGTCTCCAGACTTTCAGTCTGTGACTCCAAAAGAGA
AAGTCACCATCACCTGCAGGGCCAGTCAGTTCGTTGGCTCAAGCATCCACTG
GTACCAGCAGAAGCCAGATCAGTCTCCAAAGCTCCTCATCAAGTATGCTTCT
GAGTCTATGTCTGGGGTCCCCTCGAGGTTCAGTGGCAGTGGATCTGGGACAG
ATTTCACCCTCACCATCAATAGCCTGGAAGCTGAAGATGCTGCCACGTATTAC
TGTCAACAAAGTCATAGCTGGCATTTCACGTTCGGCCAAGGGACCAAGGTGG
AAATCAAA

FIGURE 2.

A.

SEQ ID NO:3 - Hu1 heavy chain variable region amino acid sequence

EVQLVESGGGLVQPGGSLRLSCAASGFTFSNHWMNWVRQAPGKGLEWVGEIRS
KSINSATHYAESVKGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCARNYYGSTY
DHWGQGTLVTVSS

B.

SEQ ID NO:4 - Hu1 heavy chain variable region nucleic acid sequence

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGAGGGTCCC
TGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTCAGTAACCACTGGATGAAC
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGGCGAAATTAGAT
CAAAATCTATTAATTCTGCAACACATTATGCGGAGTCTGTGAAAGGGAGATT
CACCATCTCAAGAGATGATTCAAAGAACTCACTGTACCTGCAGATGAACAGC
CTGAAAACCGAGGACACGGCCGTGTATTACTGTGCTAGAAATTACTACGGTA
GTACCTACGACCATTGGGGCCAAGGGACCCTGGTCACCGTCTCCTCA

FIGURE 3

A.

SEQ ID NO:5 - A10K light chain variable region amino acid sequence

EIVLTQSPDFQSVTPKEKVTITCRASQFVGYSIHWYQQKPDQSPKLLIKYASESRS
GVPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSHSWHFTFGQGTKVEIK

B.

SEQ ID NO:6 - A10K light chain variable region nucleic acid sequence

GAAATTGTGCTGACTCAGTCTCCAGACTTTCAGTCTGTGACTCCAAAAGAGA
AAGTCACCATCACCTGCAGGGCCAGTCAGTTCGTTGGCTATAGCATCCACTG
GTACCAGCAGAAGCCAGATCAGTCTCCAAAGCTCCTCATCAAGTATGCTTCT
GAGTCTAGGTCTGGGGTCCCCTCGAGGTTCAGTGGCAGTGGATCTGGGACAG
ATTTCACCCTCACCATCAATAGCCTGGAAGCTGAAGATGCTGCCACGTATTAC
TGTCAACAAAGTCATAGCTGGCATTTCACGTTCGGCCAAGGGACCAAGGTGG
AAATCAAA

FIGURE 4

A.

SEQ ID NO:7 - A10K heavy chain amino acid sequence

EVQLVESGGGLVQPGGSLRLSCAASGFKFSNHWMNWVRQAPGKGLEWVGEIRS
KSMNSATHYAESVKGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCARNYYGST
YDHWGQGTLVTVSS

B.

SEQ ID NO:8 - A10K heavy chain nucleic acid sequence

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGAGGGTCCC
TGAGACTCTCCTGTGCAGCCTCTGGATTCCCTTTCAGTAACCACTGGATGAAC
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGGCGAAATTAGAT
CAAAATCTATGAATTCTGCAACACATTATGCGGAGTCTGTGAAAGGGAGATT
CACCATCTCAAGAGATGATTCAAAGAACTCACTGTACCTGCAGATGAACAGC
CTGAAAACCGAGGACACGGCCGTGTATTACTGTGCTAGAAATTACTACGGTA
GTACCTACGACCATTGGGGCCAAGGGACCCTGGTCACCGTCTCCTCA

FIGURE 5

A.   Amino acid sequence of a human light chain framework region with
      interspersed CDR sequences labeled

```
   (FRL1 - SEQ ID NO:57)                (CDRL1)        (FRL2 - SEQ ID NO:58)     (CDRL2)
EIVLTQSPDFQSVTPKEKVTITCXXXXXXXXXXXXWYQQKPDQSPKLLIKXXXXXXXX

        (FRL3 - SEQ ID NO:59)                    (CDRL3)       (FRL4 - SEQ ID NO:60)
GVPSRFSGSGSGTDFTLTINSLEAEDAATYYCXXXXXXXXXXFGQGTKVEIK
```

B.   Nucleic acid sequence of a human light chain framework region with
      interspersed CDR sequences labeled

```
             (FRL1 - SEQ ID NO:61)
GAAATTGTGCTGACTCAGTCTCCAGACTTTCAGTCTGTGACTCCAAAAGAGAAAG

                                          (CDRL1)
TCACCATCACCTGCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTGGTAC

        (FRL2 - SEQ ID NO:62)                              (CDRL2)
CAGCAGAAGCCAGATCAGTCTCCAAAGCTCCTCATCAAGXXXXXXXXXXXXXXX

(CDRL2 cont.)                      (FRL3 - SEQ ID NO:63)
XXXXXXXGGGGTCCCCTCGAGGTTCAGTGGCAGTGGATCTGGGACAGATTTCAC

CCTCACCATCAATAGCCTGGAAGCTGAAGATGCTGCCACGTATTACTGT

            (CDRL3)                              (FRL4 - SEQ ID NO:64)
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTTCGGCCAAGGGACCAAGGTGGAAA

TCAAA
```

FIGURE 6

A. Amino acid sequence of a human heavy chain framework region with interspersed CDR sequences labeled

(FRH1 - SEQ ID NO:65)   (CDRH1)   (FRH2 - SEQ ID NO:66)
EVQLVESGGGLVQPGGSLRLSCAAS<u>XXXXXXXXXXX</u>WVRQAPGKGLEWVG

(CDRH2)   (FRH3 - SEQ ID NO:67)
<u>XXXXXXXXXXXXXXXXXXXX</u>RFTISRDDSKNSLYLQMNSLKTEDTAVYYCAR

(CDRH3)   (FRH4 - SEQ ID NO:68)
<u>XXXXXXXXX</u>WGQGTLVTVSS

B. Nucleic acid sequence of a human heavy chain framework region with interspersed CDR sequences labeled

(FRH1 - SEQ ID NO:69)
GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGAGGGTCCCTG

(CDRH1)
AGACTCTCCTGTGCAGCCTCT<u>XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX</u>TG

(FRH2 - SEQ ID NO:70)   (CDRH2)
GGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGGC<u>XXXXXXXXXXXXXX</u>

(CDRH2 cont.)
<u>XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX</u>AGATTCAC

(FRH3 - SEQ ID NO:71)
CATCTCAAGAGATGATTCAAAGAACTCACTGTACCTGCAGATGAACAGCCTGAA

(CDRH3)
AACCGAGGACACGGCCGTGTATTACTGTGCTAGA<u>XXXXXXXXXXXXXXXXXXXXXX</u>

(CDRH3)   (FRH4 - SEQ ID NO:72)
<u>XXXXXXXX</u>TGGGGCCAAGGGACCCTGGTCACCGTCTCCTCA

FIGURE 7

Elisa Assay
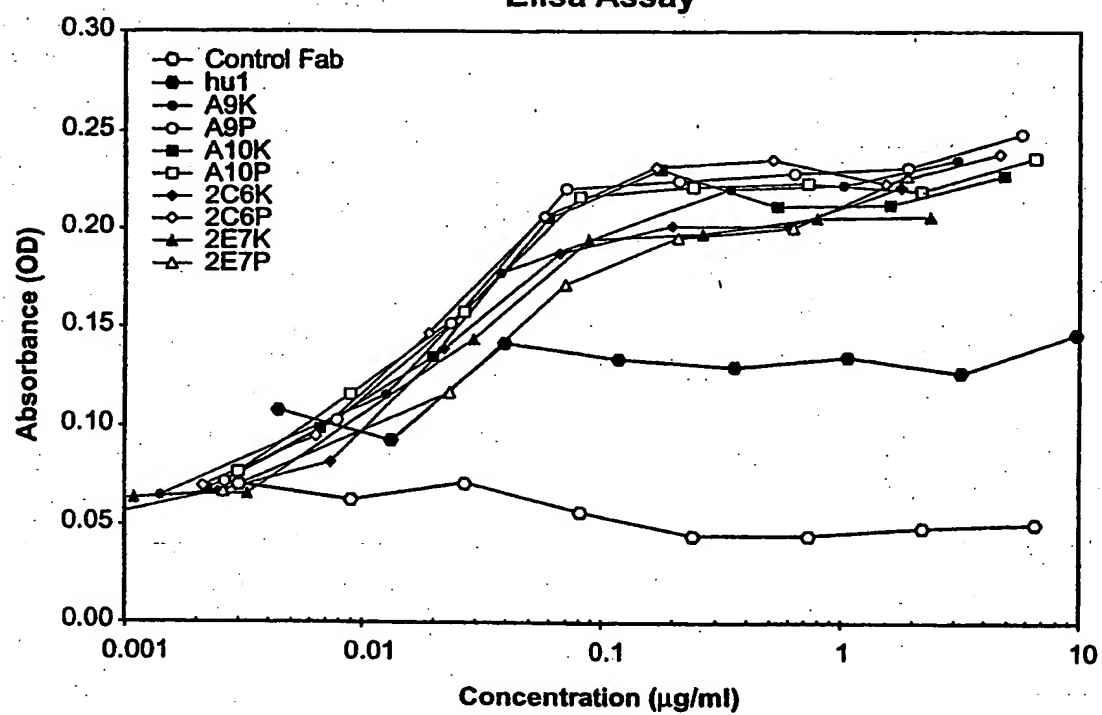
FIGURE 8

L929 Assay
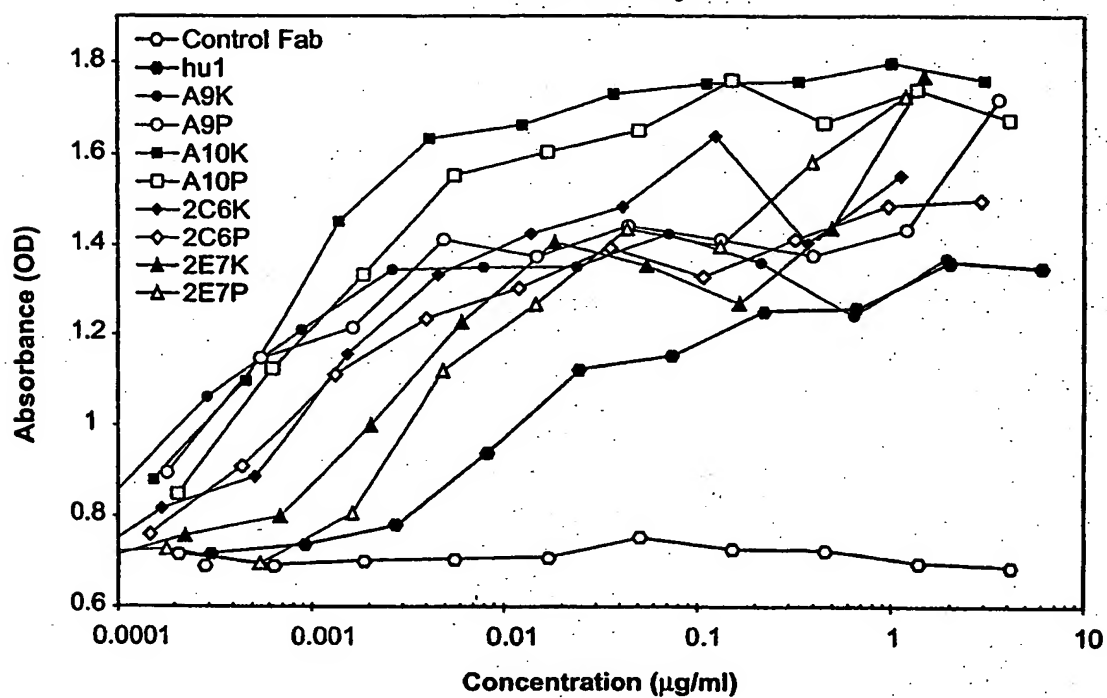
FIGURE 9
L929 Assay
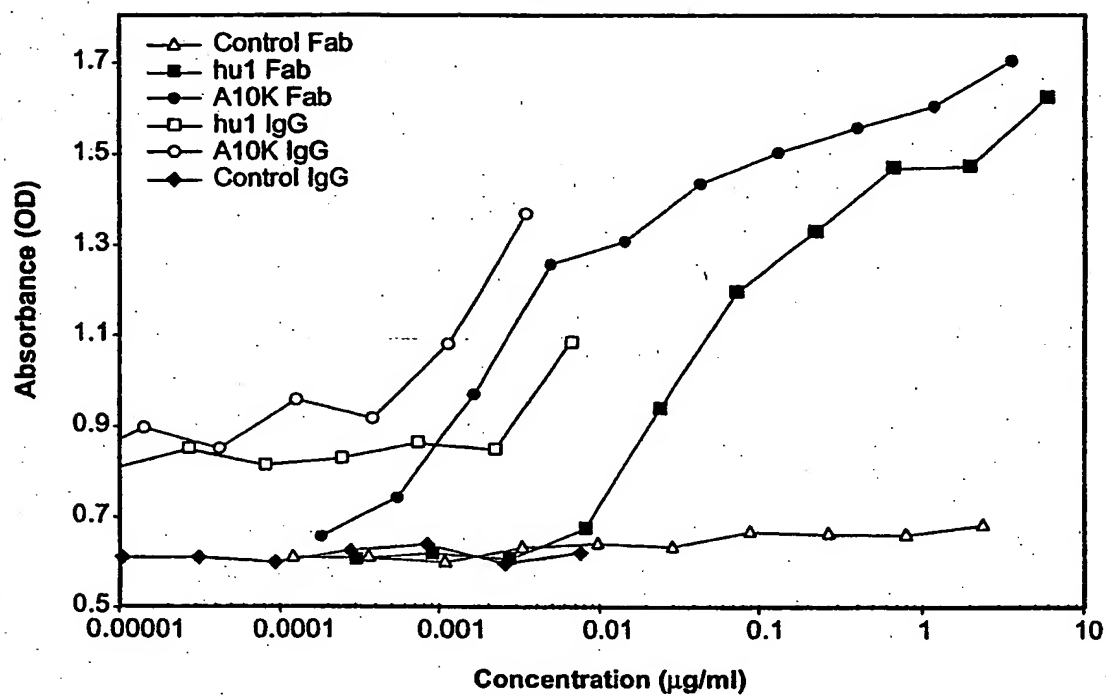
FIGURE 10
L929 Assay
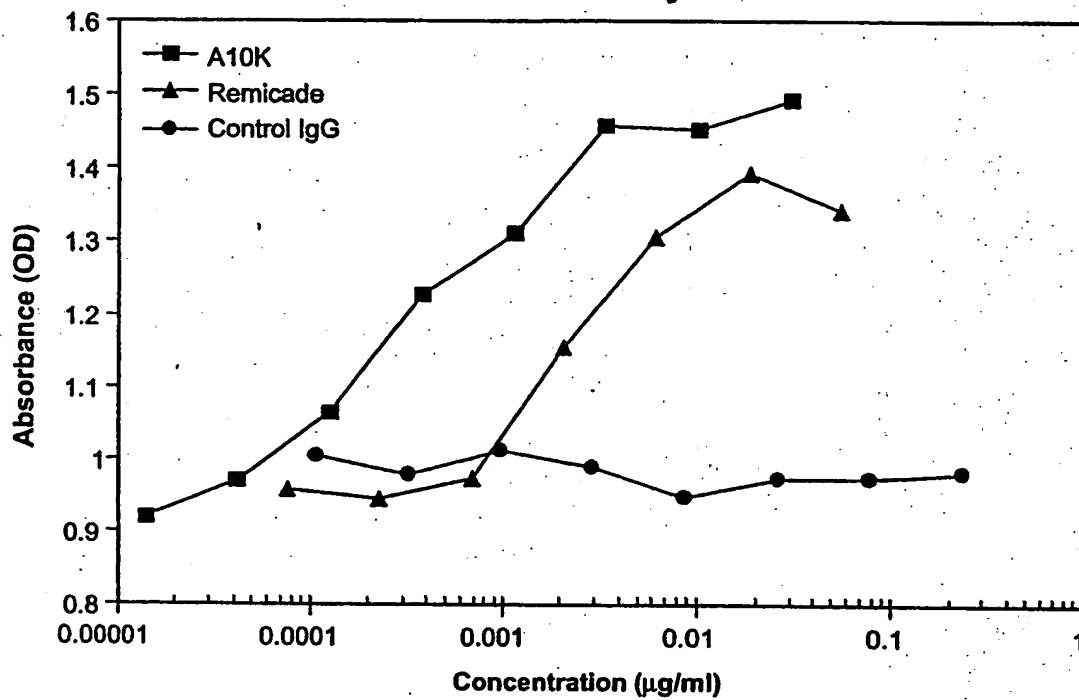
FIGURE 11
Lethality Model
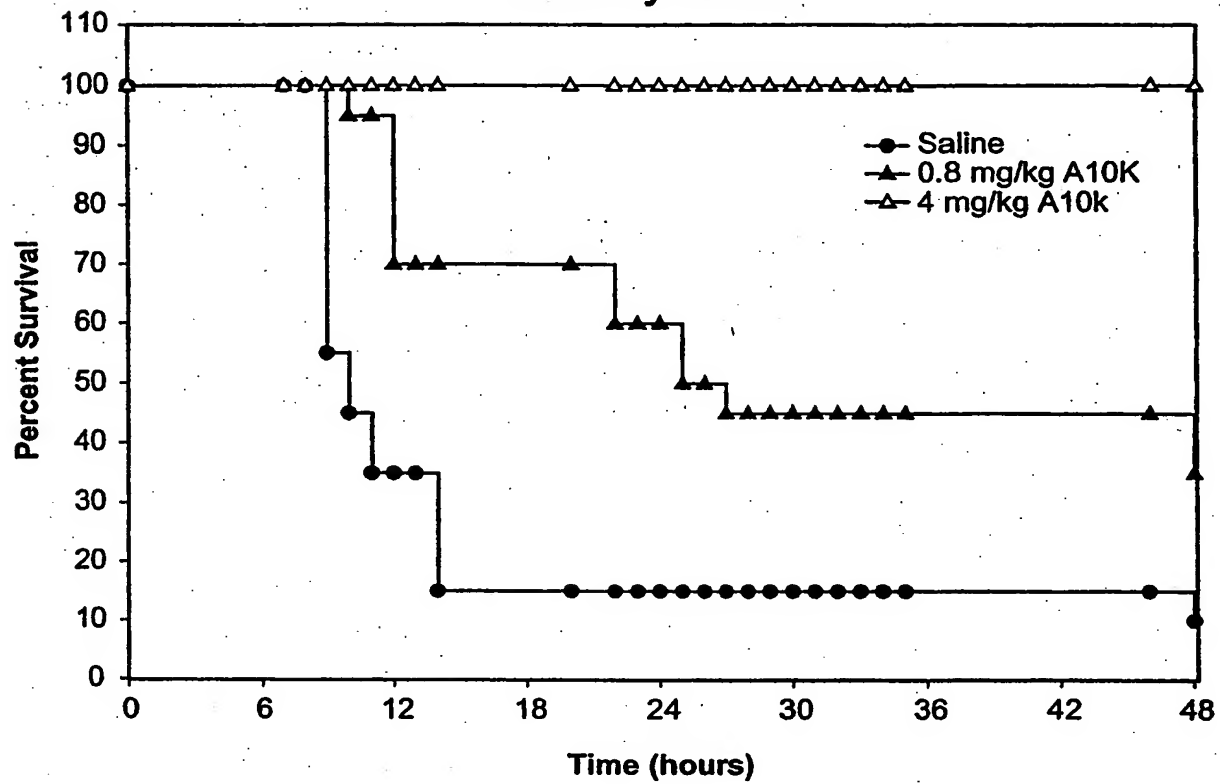
FIGURE 12
Polyarthritis Model
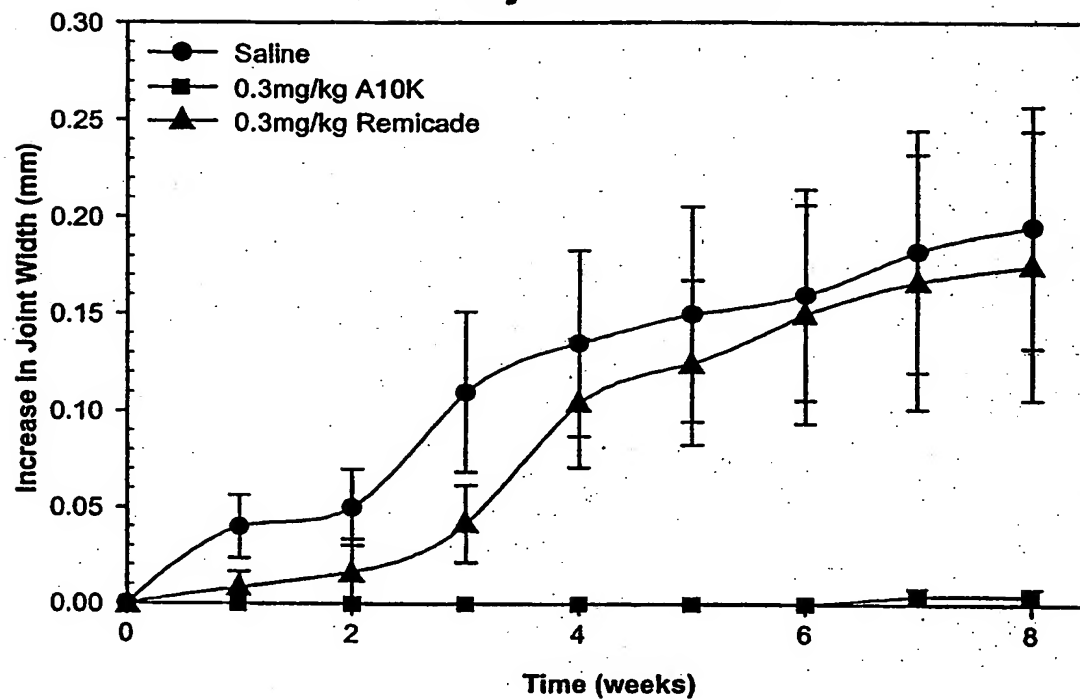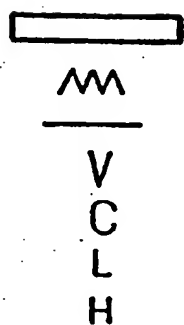
FIGURE 13

	domains
⋀⋀⋀	inter-domain sections
———	disulphide bonds
V	variable
C	constant
L	light chain
H	heavy chain

XCID: <WO_____2004063335A2_I_>

FIGURE 14

A.   SEQ ID NO:85 - Human CL Sequence

TCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAG
CACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACA
CCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTG
ACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATC
ACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAGAGCCC**AAATCTTCT**
<u>ACTAGTGTTCTC</u>*TACCCATATGATGTACCTGATTATGCATCA*TAG

Note: This CH1 sequence contains the first six IgG1 hinge region residues (in bold) and fused to a HA decapeptide tag (italic) through a four amino acid linker (underlined).

B.   SEQ ID NO:86 - Human CH1 Sequence

CGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
GAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAG
AGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCA
GGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAG
CACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGC
GAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG
GAGAGTCTTAG

FIGURE 15

A.

SEQ ID NO:109 - AME 3-2 Complete Heavy Chain

EVQLVESGGGLVQPGGSLRLSCAASGFTFRNHWMNWVRQAPGKGLEWVGEIR
SKSINSATFYAESVKGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCARNYYGSY
YDHWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD
KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK*

B.

SEQ ID NO:110 - AME 3-2 Complete Light Chain

DIQMTQSPSSLSASVGDRVTITCVTTQFVGYAIHWYQQKPGKAPKLLIYYASSSR
SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHGWPFTFGQGTKVEIKRTV
AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT
EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC*